

SEQUENCE LISTING

<110> Deng, Ming-De
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 Wassink, Sarah

<120> Process and Materials for Production of Glucosamine and N-Acetyl Glucosamine

<130> 3161-18-2

<150> 60/393,348
 <151> 2002-07-01

<160> 137

<170> PatentIn version 3.1

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Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
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Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
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Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
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His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
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Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
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Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
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His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
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Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
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Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
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His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
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Gly Leu Ala Val Val Asp Thr Glu Gly His Met Thr Arg Leu Arg Arg
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Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
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His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
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gcc gat atg ccg gtt att gtt gtc ccg aac aac gaa ttg ctg gaa Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu 515 520 525	1584
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Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys	
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ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt	1824
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 35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
 100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
 115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
 130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
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Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
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Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
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Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
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Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
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Glu

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 Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
 20 25 30

 ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144
 Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
 35 40 45

 ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192
 Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60

 cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa 240
 His Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80

 cct tca gaa gtg aat gcg cat ccg cat gtt tcc gaa cac att gtg gtg 288
 Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95

 gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta 336
 Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
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 aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att 384
 Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
 115 120 125

 gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag 432
 Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
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 Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
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 Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
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 agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct 576
 Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
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gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu 405 410 415	1248
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ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val 595 600 605	1824
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35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
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Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
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Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Pro Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
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Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
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ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

48

96

144

192

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu 65 70 75 80	240
cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val 85 90 95	288
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tac acc gtt ccg ctg cag ctg gct tac cat gtc gcg ctg atc aaa Tyr Thr Val Pro Leu Gln Leu Ala Tyr His Val Ala Leu Ile Lys 580 585 590	1776
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val 595 600 605	1824
gag taa Glu	1830

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<400> 10

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Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

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 <213> Escherichia coli

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 ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
 Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
 20 25 30

 ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144
 Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
 35 40 45

 ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192
 Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60

 cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa 240
 His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80

 cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg 288
 Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95

 gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta 336
 Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
 100 105 110

 aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att 384
 Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
 115 120 125

 gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag 432
 Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
 130 135 140

 gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac qgt aca qtg 480
 Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
 145 150 155 160

 atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct qgt 528
 Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
 165 170 175

agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser 180 185 190	576
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu 195 200 205	624
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp 210 215 220	672
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln 225 230 235 240	720
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu 245 250 255	768
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile 260 265 270	816
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu 275 280 285	864
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser 290 295 300	912
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly 305 310 315 320	960
att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser 325 330 335	1008
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu 340 345 350	1056
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr 355 360 365	1104
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg 370 375 380	1152
gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val 385 390 395 400	1200
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu 405 410 415	1248

gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His 420 425 430	1296
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met 435 440 445	1344
ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp 450 455 460	1392
aaa cat cac gcg ctg ttc ctg agc cgt ggc gat cag tac cca atc gcg Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala 465 470 475 480	1440
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu 485 490 495	1488
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp 500 505 510	1536
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu 515 520 525	1584
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu 530 535 540	1632
tat gtc ttc gcc gat ccg cat gat gcg ggt ttt gta agt agc gat aac atg Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met 545 550 555 560	1680
cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe 565 570 575	1728
tac acc gtt ccg ctg cag ctg gct tac cat gtc gcg ctg atc aaa Tyr Thr Val Pro Leu Gln Leu Ala Tyr His Val Ala Leu Ile Lys 580 585 590	1776
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val 595 600 605	1824
gag taa Glu	1830

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<212> PRT
<213> Escherichia coli
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Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
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Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

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ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu 50 55 60	192
cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu 65 70 75 80	240
cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val 85 90 95	288
gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu 100 105 110	336
aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile 115 120 125	384
gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Thr Leu Arg Glu 130 135 140	432
gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtc Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val 145 150 155 160	480
atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly 165 170 175	528
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser 180 185 190	576
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa Asp Gln Leu Ala Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu 195 200 205	624
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp 210 215 220	672
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln 225 230 235 240	720
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu 245 250 255	768
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile 260 265 270	816
agc cac ggt cag gtt gat tta agc gag ctg gga cgc aac gcc gac gaa Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu 275 280 285	864

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tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly 305 310 315 320	960
att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser 325 330 335	1008
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu 340 345 350	1056
acc gcg gat acc ctg gct ggc ctg cgt ctg aaa gag ctg ggt tac Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr 355 360 365	1104
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg 370 375 380	1152
gaa tcc gtt ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg Glu Ser Val Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val 385 390 395 400	1200
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu 405 410 415	1248
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His 420 425 430	1296
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met 435 440 445	1344
ctg cct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac Leu Pro Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp 450 455 460	1392
aaa cat cac gcg ctg ttc ctg ggc cgt ggc gat cag tac cca atc gcg Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala 465 470 475 480	1440
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu 485 490 495	1488
gcc tac gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp 500 505 510	1536
gcc gat atg ccg gtt att gtt gca ccg aac aac gga ttg ctg gaa Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Gly Leu Leu Glu 515 520 525	1584

aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg	1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu	
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tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg	1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met	
545 550 555 560	
cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc	1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe	
565 570 575	
tac acc gtt ccg ctg cag ctg gct tac cat gtc gcg ctg atc aaa	1776
Tyr Thr Val Pro Leu Gln Leu Ala Tyr His Val Ala Leu Ile Lys	
580 585 590	
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt	1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val	
595 600 605	
gag taa	1830
Glu	

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 <211> 609
 <212> PRT
 <213> Escherichia coli

<400> 14

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Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
 35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
 100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Val Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Pro Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Gly Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

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tta tta aaa ggg tta gag aag ctt gag tat cgc ggt tat gac tct gct 96
Leu Leu Lys Gly Leu Glu Lys Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30
ggt att gct gtt gcc aac gaa cag gga atc cat gtc ttc aaa gaa aaa 144
Gly Ile Ala Val Ala Asn Glu Gln Gly Ile His Val Phe Lys Glu Lys
35 40 45
gga cgc att gca gat ctt cgt gaa gtt gtc gat gcc aat gta gaa gcg 192
Gly Arg Ile Ala Asp Leu Arg Glu Val Val Asp Ala Asn Val Glu Ala
50 55 60
aaa gcc gga att ggg cat act cgc tgg gcg aca cac ggc gaa cca agc 240
Lys Ala Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Glu Pro Ser
65 70 75 80
tat ctg aac gct cac ccg cat caa agc gca ctg ggc cgc ttt aca ctt 288
Tyr Leu Asn Ala His Pro His Gln Ser Ala Leu Gly Arg Phe Thr Leu
85 90 95
gtt cac aac ggc gtc atc gag aac tat gtt cag ctg aag caa gag tat 336
Val His Asn Gly Val Ile Glu Asn Tyr Val Gln Leu Lys Gln Glu Tyr
100 105 110
ttg caa gat gta gag ctc aaa agt gac acc gat aca gaa gta gtc gtt 384
Leu Gln Asp Val Glu Leu Lys Ser Asp Thr Asp Thr Glu Val Val Val
115 120 125
caa gta atc gag caa ttc gtc aat gga gga ctt gag aca gaa gaa gcg 432
Gln Val Ile Glu Gln Phe Val Asn Gly Gly Leu Glu Thr Glu Glu Ala
130 135 140
ttc cgc aaa aca ctt aca ctg tta aaa ggc tct tat gca att gct tta 480
Phe Arg Lys Thr Leu Thr Leu Lys Gly Ser Tyr Ala Ile Ala Leu
145 150 155 160

ttc gat aac gac aac aga gaa acg att ttt gta gcg aaa aac aaa agc Phe Asp Asn Asp Asn Arg Glu Thr Ile Phe Val Ala Lys Asn Lys Ser 165 170 175	528
cct cta tta gta ggt ctt gga gat aca ttc aac gtc gta gca tct gat Pro Leu Leu Val Gly Leu Gly Asp Thr Phe Asn Val Val Ala Ser Asp 180 185 190	576
gcg atg gcg atg ctt caa gta acc aac gaa tac gta gag ctg atg gat Ala Met Ala Met Leu Gln Val Thr Asn Glu Tyr Val Glu Leu Met Asp 195 200 205	624
aaa gaa atg gtt atc gtc act gat gac caa gtt gtc atc aaa aac ctt Lys Glu Met Val Ile Val Thr Asp Asp Gln Val Val Ile Lys Asn Leu 210 215 220	672
gat ggt gac gtg att aca cgt gcg tct tat att gct gag ctt gat gcc Asp Gly Asp Val Ile Thr Arg Ala Ser Tyr Ile Ala Glu Leu Asp Ala 225 230 235 240	720
agt gat atc gaa aaa ggc acg tac cct cac tac atg ttg aaa gaa acg Ser Asp Ile Glu Lys Gly Thr Tyr Pro His Tyr Met Leu Lys Glu Thr 245 250 255	768
gat gag cag cct gtt gtt atg cgc aaa atc atc caa acg tat caa gat Asp Glu Gln Pro Val Val Met Arg Lys Ile Ile Gln Thr Tyr Gln Asp 260 265 270	816
gaa aac ggc aag ctg tct gtg cct ggc gat atc gct gcc gct gta gcg Glu Asn Gly Lys Leu Ser Val Pro Gly Asp Ile Ala Ala Val Ala 275 280 285	864
gaa gcg gac cgc atc tat atc att ggc tgc gga aca agc tac cat gca Glu Ala Asp Arg Ile Tyr Ile Ile Gly Cys Gly Thr Ser Tyr His Ala 290 295 300	912
gga ctt gtc ggt aaa caa tat att gaa atg tgg gca aac gtg ccg gtt Gly Leu Val Gly Lys Gln Tyr Ile Glu Met Trp Ala Asn Val Pro Val 305 310 315 320	960
gaa gtg cat gta gcg agt gaa ttc tcc tac aac atg ccg ctt ctg tct Glu Val His Val Ala Ser Glu Phe Ser Tyr Asn Met Pro Leu Leu Ser 325 330 335	1008
aag aaa ccg ctc ttc att ttc ctt tct caa agc gga gaa aca gca gac Lys Lys Pro Leu Phe Ile Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp 340 345 350	1056
agc cgc gcg gta ctc gtt caa gtc aaa gcg ctc gga cac aaa gcc ctg Ser Arg Ala Val Leu Val Gln Val Lys Ala Leu Gly His Lys Ala Leu 355 360 365	1104
aca atc aca aac gta cct gga tca acg ctt tct cgt gaa gct gac tat Thr Ile Thr Asn Val Pro Gly Ser Thr Leu Ser Arg Glu Ala Asp Tyr 370 375 380	1152
aca ttg ctg ctt cat gca ggc cct gag atc gct gtt gcg tca acg aaa Thr Leu Leu Leu His Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys 385 390 395 400	1200

gca tac act gca caa atc gca gtt ctg gcg gtt ctt gct tct gtg gct Ala Tyr Thr Ala Gln Ile Ala Val Leu Ala Val Leu Ala Ser Val Ala 405 410 415	1248
gct gac aaa aat ggc atc aat atc gga ttt gac ctc gtc aaa gaa ctc Ala Asp Lys Asn Gly Ile Asn Ile Gly Phe Asp Leu Val Lys Glu Leu 420 425 430	1296
ggt atc gct gca aac gca atg gaa gct cta tgc gac cag aaa gac gaa Gly Ile Ala Ala Asn Ala Met Glu Ala Leu Cys Asp Gln Lys Asp Glu 435 440 445	1344
atg gaa atg atc gct cgt gaa tac ctg act gta tcc aga aat gct ttc Met Glu Met Ile Ala Arg Glu Tyr Leu Thr Val Ser Arg Asn Ala Phe 450 455 460	1392
ttc atc gga cgc ggc ctt gac tac ttc gta tgt gtc gaa ggc gca ctg Phe Ile Gly Arg Gly Leu Asp Tyr Phe Val Cys Val Glu Gly Ala Leu 465 470 475 480	1440
aag ctg aaa gag att tct tac atc cag gca gaa ggt ttt gcc ggc ggt Lys Leu Lys Glu Ile Ser Tyr Ile Gln Ala Glu Gly Phe Ala Gly Gly 485 490 495	1488
gag cta aag cac gga acg att gcc ttg atc gaa caa gga aca cca gta Glu Leu Lys His Gly Thr Ile Ala Leu Ile Glu Gln Gly Thr Pro Val 500 505 510	1536
ttc gca ctg gca act caa gag cat gta aac cta agc atc cgc gga aac Phe Ala Leu Ala Thr Gln Glu His Val Asn Leu Ser Ile Arg Gly Asn 515 520 525	1584
gtc aaa gaa gtt gct gct cgc gga gca aac aca tgc atc atc tca ctg Val Lys Glu Val Ala Ala Arg Gly Ala Asn Thr Cys Ile Ile Ser Leu 530 535 540	1632
aaa ggc cta gac gat gcg gat gac aga ttc gta ttg ccg gaa gta aac Lys Gly Leu Asp Asp Ala Asp Asp Arg Phe Val Leu Pro Glu Val Asn 545 550 555 560	1680
cca gcg ctt gct ccg ttg gta tct gtt cca ttg cag ctg atc gct Pro Ala Leu Ala Pro Leu Val Ser Val Val Pro Leu Gln Leu Ile Ala 565 570 575	1728
tac tat gct gca ctg cat cgc ggc tgt gat gtg gat aaa cct cgt aac Tyr Tyr Ala Ala Leu His Arg Gly Cys Asp Val Asp Lys Pro Arg Asn 580 585 590	1776
ctt gcg aag agt gtt act gtg gag taa Leu Ala Lys Ser Val Thr Val Glu 595 600	1803

<210> 16
 <211> 600
 <212> PRT
 <213> *Bacillus subtilis*

<400> 16

Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Leu Asp Ala Lys Glu Ile
1 5 10 15

Leu Leu Lys Gly Leu Glu Lys Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

Gly Ile Ala Val Ala Asn Glu Gln Gly Ile His Val Phe Lys Glu Lys
35 40 45

Gly Arg Ile Ala Asp Leu Arg Glu Val Val Asp Ala Asn Val Glu Ala
50 55 60

Lys Ala Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Glu Pro Ser
65 70 75 80

Tyr Leu Asn Ala His Pro His Gln Ser Ala Leu Gly Arg Phe Thr Leu
85 90 95

Val His Asn Gly Val Ile Glu Asn Tyr Val Gln Leu Lys Gln Glu Tyr
100 105 110

Leu Gln Asp Val Glu Leu Lys Ser Asp Thr Asp Thr Glu Val Val Val
115 120 125

Gln Val Ile Glu Gln Phe Val Asn Gly Gly Leu Glu Thr Glu Glu Ala
130 135 140

Phe Arg Lys Thr Leu Thr Leu Lys Gly Ser Tyr Ala Ile Ala Leu
145 150 155 160

Phe Asp Asn Asp Asn Arg Glu Thr Ile Phe Val Ala Lys Asn Lys Ser
165 170 175

Pro Leu Leu Val Gly Leu Gly Asp Thr Phe Asn Val Val Ala Ser Asp
180 185 190

Ala Met Ala Met Leu Gln Val Thr Asn Glu Tyr Val Glu Leu Met Asp
195 200 205

Lys Glu Met Val Ile Val Thr Asp Asp Gln Val Val Ile Lys Asn Leu
210 215 220

Asp Gly Asp Val Ile Thr Arg Ala Ser Tyr Ile Ala Glu Leu Asp Ala
225 230 235 240

Ser Asp Ile Glu Lys Gly Thr Tyr Pro His Tyr Met Leu Lys Glu Thr
245 250 255

Asp Glu Gln Pro Val Val Met Arg Lys Ile Ile Gln Thr Tyr Gln Asp
260 265 270

Glu Asn Gly Lys Leu Ser Val Pro Gly Asp Ile Ala Ala Ala Val Ala
275 280 285

Glu Ala Asp Arg Ile Tyr Ile Ile Gly Cys Gly Thr Ser Tyr His Ala
290 295 300

Gly Leu Val Gly Lys Gln Tyr Ile Glu Met Trp Ala Asn Val Pro Val
305 310 315 320

Glu Val His Val Ala Ser Glu Phe Ser Tyr Asn Met Pro Leu Leu Ser
325 330 335

Lys Lys Pro Leu Phe Ile Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp
340 345 350

Ser Arg Ala Val Leu Val Gln Val Lys Ala Leu Gly His Lys Ala Leu
355 360 365

Thr Ile Thr Asn Val Pro Gly Ser Thr Leu Ser Arg Glu Ala Asp Tyr
370 375 380

Thr Leu Leu Leu His Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys
385 390 395 400

Ala Tyr Thr Ala Gln Ile Ala Val Leu Ala Val Leu Ala Ser Val Ala
405 410 415

Ala Asp Lys Asn Gly Ile Asn Ile Gly Phe Asp Leu Val Lys Glu Leu
420 425 430

Gly Ile Ala Ala Asn Ala Met Glu Ala Leu Cys Asp Gln Lys Asp Glu
435 440 445

Met Glu Met Ile Ala Arg Glu Tyr Leu Thr Val Ser Arg Asn Ala Phe
450 455 460

Phe Ile Gly Arg Gly Leu Asp Tyr Phe Val Cys Val Glu Gly Ala Leu
465 470 475 480

Lys Leu Lys Glu Ile Ser Tyr Ile Gln Ala Glu Gly Phe Ala Gly Gly
485 490 495

Glu Leu Lys His Gly Thr Ile Ala Leu Ile Glu Gln Gly Thr Pro Val
500 505 510

Phe Ala Leu Ala Thr Gln Glu His Val Asn Leu Ser Ile Arg Gly Asn
515 520 525

Val Lys Glu Val Ala Ala Arg Gly Ala Asn Thr Cys Ile Ile Ser Leu
530 535 540

Lys Gly Leu Asp Asp Ala Asp Asp Arg Phe Val Leu Pro Glu Val Asn
545 550 555 560

Pro Ala Leu Ala Pro Leu Val Ser Val Val Pro Leu Gln Leu Ile Ala
565 570 575

Tyr Tyr Ala Ala Leu His Arg Gly Cys Asp Val Asp Lys Pro Arg Asn
580 585 590

Leu Ala Lys Ser Val Thr Val Glu
595 600

<210> 17

<211> 2154

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

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<223>

<400> 17

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Met Cys Gly Ile Phe Gly Tyr Cys Asn Tyr Leu Val Glu Arg Ser Arg
1 5 10 15

gga gaa att atc gac acc tta gtg gat ggt tta caa aga tta gaa tat 96
Gly Glu Ile Ile Asp Thr Leu Val Asp Gly Leu Gln Arg Leu Glu Tyr
20 25 30

aga ggc tat gat tcc acc ggt att gct atc gat ggt gac gaa gct gat 144
Arg Gly Tyr Asp Ser Thr Gly Ile Ala Ile Asp Gly Asp Glu Ala Asp
35 40 45

tct act ttc atc tat aag caa atc ggt aaa gtg agt gct ttg aaa gag 192
Ser Thr Phe Ile Tyr Lys Gln Ile Gly Lys Val Ser Ala Leu Lys Glu
50 55 60

gag att act aag caa aat ccg aac aga gac gtt act ttt gtc tct cat Glu Ile Thr Lys Gln Asn Pro Asn Arg Asp Val Thr Phe Val Ser His 65 70 75 80	240
tgt ggt att gcg cat act aga tgg gct act cac ggt cga cca gaa caa Cys Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Arg Pro Glu Gln 85 90 95	288
gtt aac tgt cac cct caa aga tct gac cca gaa gac caa ttt gtg gtc Val Asn Cys His Pro Gln Arg Ser Asp Pro Glu Asp Gln Phe Val Val 100 105 110	336
gtt cat aat ggt atc atc aca aat ttt aga gaa ctg aag act ctt tta Val His Asn Gly Ile Ile Thr Asn Phe Arg Glu Leu Lys Thr Leu Leu 115 120 125	384
att aac aaa ggt tat aaa ttc gaa agt gat acc gat acc gag tgt att Ile Asn Lys Gly Tyr Lys Phe Glu Ser Asp Thr Asp Thr Glu Cys Ile 130 135 140	432
gct aaa cta tat ttg cat tta tac aat aca aat tta caa aat ggg cat Ala Lys Leu Tyr Leu His Leu Tyr Asn Thr Asn Leu Gln Asn Gly His 145 150 155 160	480
gac tta gat ttc cac gaa tta acc aag cta gtt ctt tta gaa cta gaa Asp Leu Asp Phe His Glu Leu Thr Lys Leu Val Leu Glu Leu Glu 165 170 175	528
ggt tca tac ggg tta tta tgt aaa tct tgt cac tat cct aat gag gtt Gly Ser Tyr Gly Leu Leu Cys Lys Ser Cys His Tyr Pro Asn Glu Val 180 185 190	576
atc gcc act aga aaa ggg tcc cct tta ctg att ggt gtc aaa tct gaa Ile Ala Thr Arg Lys Gly Ser Pro Leu Leu Ile Gly Val Lys Ser Glu 195 200 205	624
aaa aaa cta aaa gtc gac ttc gtg gat gtg gaa ttt ccc gaa gaa aac Lys Lys Leu Lys Val Asp Phe Val Asp Val Glu Phe Pro Glu Glu Asn 210 215 220	672
gct ggt caa ccg gaa att cca ttg aaa tct aac aac aaa tca ttt ggc Ala Gly Gln Pro Glu Ile Pro Leu Lys Ser Asn Asn Lys Ser Phe Gly 225 230 235 240	720
ttg ggc cca aag aaa gct cgt gaa ttt gaa gct ggt tcc caa aat gcc Leu Gly Pro Lys Lys Ala Arg Glu Phe Ala Gly Ser Gln Asn Ala 245 250 255	768
aat tta cta cca att gcc gcc aat gaa ttt aac ttg aga cat tct caa Asn Leu Leu Pro Ile Ala Ala Asn Glu Phe Asn Leu Arg His Ser Gln 260 265 270	816
tcc agg gct ttc cta tca gaa gat gga tct cca aca ccg gtg gaa ttt Ser Arg Ala Phe Leu Ser Glu Asp Gly Ser Pro Thr Pro Val Glu Phe 275 280 285	864
ttt gtt tct tcg gat gcg gca tct gtt aaa cat acc aag aag gtg Phe Val Ser Ser Asp Ala Ala Ser Val Val Lys His Thr Lys Lys Val 290 295 300	912

ctt ttt tta gaa gat gac gat ttg gct cat att tac gat ggt gag tta Leu Phe Leu Glu Asp Asp Asp Leu Ala His Ile Tyr Asp Gly Glu Leu 305 310 315 320	960
cat att cat aga tct aga aga gaa gta ggc gca tca atg aca agg tcc His Ile His Arg Ser Arg Arg Glu Val Gly Ala Ser Met Thr Arg Ser 325 330 335	1008
att caa act tta gag atg gag tta gct cag atc atg aag ggc cct tac Ile Gln Thr Leu Glu Met Glu Leu Ala Gln Ile Met Lys Gly Pro Tyr 340 345 350	1056
gac cat ttt atg caa aag gaa atc tat gag caa cca gaa tct act ttc Asp His Phe Met Gln Lys Glu Ile Tyr Glu Gln Pro Glu Ser Thr Phe 355 360 365	1104
aat act atg aga ggt aga atc gac tat gaa aat aat aaa gtg ata ttg Asn Thr Met Arg Gly Arg Ile Asp Tyr Glu Asn Asn Lys Val Ile Leu 370 375 380	1152
ggg ggt tta aag gca tgg tta cca gtt gtc aga aga gca cgg aga ctg Gly Gly Leu Lys Ala Trp Leu Pro Val Val Arg Arg Ala Arg Arg Leu 385 390 395 400	1200
atc atg atc gca tgc ggt act tct tat cat tca tgt ttg gct act cgt Ile Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg 405 410 415	1248
gct atc ttc gaa gaa tta tca gat atc cca gtt agt gtg gaa tta gcg Ala Ile Phe Glu Glu Leu Ser Asp Ile Pro Val Ser Val Glu Leu Ala 420 425 430	1296
tct gac ttt ctg gac aga aaa tgc cct gtc ttc aga gac gat gta tgc Ser Asp Phe Leu Asp Arg Lys Cys Pro Val Phe Arg Asp Asp Val Cys 435 440 445	1344
gtg ttt gtt tca caa agt ggt gaa act gcg gat acc atg ctg gct cta Val Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Thr Met Leu Ala Leu 450 455 460	1392
aat tat tgt tta gaa aga gga gcc tta act gtc gga att gtt aac agt Asn Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser 465 470 475 480	1440
gtt ggt tct tct atc tct cgt gtc acc cac tgt ggt gtt cat att aac Val Gly Ser Ser Ile Ser Arg Val Thr His Cys Gly Val His Ile Asn 485 490 495	1488
gct ggt cct gaa att ggt gtt gcc tct aca aaa gct tat act tcc cag Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln 500 505 510	1536
tat att gcc tta gtg atg ttt gct cta tcg ctg tca gat gac cgt gta Tyr Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asp Asp Arg Val 515 520 525	1584
tcg aaa ata gac aga aga att gaa atc att caa ggc ttg aag tta atc Ser Lys Ile Asp Arg Arg Ile Glu Ile Ile Gln Gly Leu Lys Leu Ile 530 535 540	1632

ccg ggc caa att aag cag gta tta aag ctg gaa cca aga ata aaa aag Pro Gly Gln Ile Lys Gln Val Leu Lys Leu Glu Pro Arg Ile Lys Lys 545 550 555 560	1680
ctc tgt gcg act gaa tta aag gat caa aaa tct cta ttg tta ttg ggt Leu Cys Ala Thr Glu Leu Lys Asp Gln Lys Ser Leu Leu Leu Gly 565 570 575	1728
aga ggt tac caa ttt gct gct ctg gaa ggt gct ttg aag atc aaa Arg Gly Tyr Gln Phe Ala Ala Leu Glu Gly Ala Leu Lys Ile Lys 580 585 590	1776
gaa att tct tat atg cat tct gaa ggt gtt ttg gca ggt gag ttg aag Glu Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys 595 600 605	1824
cac ggt gtc ttg gcc ttg gtg gac gaa aac ttg cca atc att gct ttt His Gly Val Leu Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Ala Phe 610 615 620	1872
ggt acc aga gac tct cta ttc cct aaa gta gtt tcc tct att gag caa Gly Thr Arg Asp Ser Leu Phe Pro Lys Val Val Ser Ser Ile Glu Gln 625 630 635 640	1920
gtt act gca aga aag ggc cat cca att att att tgt aac gaa aat gat Val Thr Ala Arg Lys Gly His Pro Ile Ile Ile Cys Asn Glu Asn Asp 645 650 655	1968
gaa gtg tgg gcg caa aaa tct aaa tca atc gac ctg caa acc tta gaa Glu Val Trp Ala Gln Lys Ser Lys Ser Ile Asp Leu Gln Thr Leu Glu 660 665 670	2016
gtt cca caa act gtt gat tgt tta caa ggt cta att aat att att cca Val Pro Gln Thr Val Asp Cys Leu Gln Gly Leu Ile Asn Ile Ile Pro 675 680 685	2064
tta caa cta atg tca tat tgg ttg gct gtt aat aaa ggg att gat gtt Leu Gln Leu Met Ser Tyr Trp Leu Ala Val Asn Lys Gly Ile Asp Val 690 695 700	2112
gat ttt cca aga aac ttg gct aaa tct gtt acc gtc gaa taa Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu 705 710 715	2154

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 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 18

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Gly Glu Ile Ile Asp Thr Leu Val Asp Gly Leu Gln Arg Leu Glu Tyr
20 25 30

Arg Gly Tyr Asp Ser Thr Gly Ile Ala Ile Asp Gly Asp Glu Ala Asp
35 40 45

Ser Thr Phe Ile Tyr Lys Gln Ile Gly Lys Val Ser Ala Leu Lys Glu
50 55 60

Glu Ile Thr Lys Gln Asn Pro Asn Arg Asp Val Thr Phe Val Ser His
65 70 75 80

Cys Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Arg Pro Glu Gln
85 90 95

Val Asn Cys His Pro Gln Arg Ser Asp Pro Glu Asp Gln Phe Val Val
100 105 110

Val His Asn Gly Ile Ile Thr Asn Phe Arg Glu Leu Lys Thr Leu Leu
115 120 125

Ile Asn Lys Gly Tyr Lys Phe Glu Ser Asp Thr Asp Thr Glu Cys Ile
130 135 140

Ala Lys Leu Tyr Leu His Leu Tyr Asn Thr Asn Leu Gln Asn Gly His
145 150 155 160

Asp Leu Asp Phe His Glu Leu Thr Lys Leu Val Leu Leu Glu Leu Glu
165 170 175

Gly Ser Tyr Gly Leu Leu Cys Lys Ser Cys His Tyr Pro Asn Glu Val
180 185 190

Ile Ala Thr Arg Lys Gly Ser Pro Leu Leu Ile Gly Val Lys Ser Glu
195 200 205

Lys Lys Leu Lys Val Asp Phe Val Asp Val Glu Phe Pro Glu Glu Asn
210 215 220

Ala Gly Gln Pro Glu Ile Pro Leu Lys Ser Asn Asn Lys Ser Phe Gly
225 230 235 240

Leu Gly Pro Lys Lys Ala Arg Glu Phe Glu Ala Gly Ser Gln Asn Ala
245 250 255

Asn Leu Leu Pro Ile Ala Ala Asn Glu Phe Asn Leu Arg His Ser Gln
260 265 270

Ser Arg Ala Phe Leu Ser Glu Asp Gly Ser Pro Thr Pro Val Glu Phe
275 280 285

Phe Val Ser Ser Asp Ala Ala Ser Val Val Lys His Thr Lys Lys Val
290 295 300

Leu Phe Leu Glu Asp Asp Asp Leu Ala His Ile Tyr Asp Gly Glu Leu
305 310 315 320

His Ile His Arg Ser Arg Arg Glu Val Gly Ala Ser Met Thr Arg Ser
325 330 335

Ile Gln Thr Leu Glu Met Glu Leu Ala Gln Ile Met Lys Gly Pro Tyr
340 345 350

Asp His Phe Met Gln Lys Glu Ile Tyr Glu Gln Pro Glu Ser Thr Phe
355 360 365

Asn Thr Met Arg Gly Arg Ile Asp Tyr Glu Asn Asn Lys Val Ile Leu
370 375 380

Gly Gly Leu Lys Ala Trp Leu Pro Val Val Arg Arg Ala Arg Arg Leu
385 390 395 400

Ile Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg
405 410 415

Ala Ile Phe Glu Glu Leu Ser Asp Ile Pro Val Ser Val Glu Leu Ala
420 425 430

Ser Asp Phe Leu Asp Arg Lys Cys Pro Val Phe Arg Asp Asp Val Cys
435 440 445

Val Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Thr Met Leu Ala Leu
450 455 460

Asn Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser
465 470 475 480

Val Gly Ser Ser Ile Ser Arg Val Thr His Cys Gly Val His Ile Asn
485 490 495

Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln
500 505 510

Tyr Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asp Asp Arg Val
515 520 525

Ser Lys Ile Asp Arg Arg Ile Glu Ile Ile Gln Gly Leu Lys Leu Ile
530 535 540

Pro Gly Gln Ile Lys Gln Val Leu Lys Leu Glu Pro Arg Ile Lys Lys
545 550 555 560

Leu Cys Ala Thr Glu Leu Lys Asp Gln Lys Ser Leu Leu Leu Leu Gly
565 570 575

Arg Gly Tyr Gln Phe Ala Ala Ala Leu Glu Gly Ala Leu Lys Ile Lys
580 585 590

Glu Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys
595 600 605

His Gly Val Leu Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Ala Phe
610 615 620

Gly Thr Arg Asp Ser Leu Phe Pro Lys Val Val Ser Ser Ile Glu Gln
625 630 635 640

Val Thr Ala Arg Lys Gly His Pro Ile Ile Ile Cys Asn Glu Asn Asp
645 650 655

Glu Val Trp Ala Gln Lys Ser Lys Ser Ile Asp Leu Gln Thr Leu Glu
660 665 670

Val Pro Gln Thr Val Asp Cys Leu Gln Gly Leu Ile Asn Ile Ile Pro
675 680 685

Leu Gln Leu Met Ser Tyr Trp Leu Ala Val Asn Lys Gly Ile Asp Val
690 695 700

Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
705 710 715

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<211> 2142
<212> DNA
<213> Candida albicans

<220>
<221> CDS

<222> (1)..(2142)

<223>

<400> 19

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Met Cys Gly Ile Phe Gly Tyr Val Asn Phe Leu Val Asp Lys Ser Arg
1 5 10 15

48

ggt gaa atc att gat aat tta att gaa ggt ttg caa cga tta gaa tat
Gly Glu Ile Ile Asp Asn Leu Ile Glu Gly Leu Gln Arg Leu Glu Tyr
20 25 30

96

aga ggt tat gat tca gca ggc att gct gtt gat ggg aaa tta act aaa
Arg Gly Tyr Asp Ser Ala Gly Ile Ala Val Asp Gly Lys Leu Thr Lys
35 40 45

144

gat cct tct aat ggt gat gaa gaa tat atg gat tct att att gtt aaa
Asp Pro Ser Asn Gly Asp Glu Glu Tyr Met Asp Ser Ile Ile Val Lys
50 55 60

192

act act ggt aaa gtt aaa gtt ttg aaa caa aaa atc att gat gat caa
Thr Thr Gly Lys Val Lys Val Leu Lys Gln Lys Ile Ile Asp Asp Gln
65 70 75 80

240

atc gat aga tcg gcc att ttt gat aat cat gtt ggt att gct cat act
Ile Asp Arg Ser Ala Ile Phe Asp Asn His Val Gly Ile Ala His Thr
85 90 95

288

aga tgg gct aca cat ggt caa cca aaa act gaa aat tgt cat cct cat
Arg Trp Ala Thr His Gly Gln Pro Lys Thr Glu Asn Cys His Pro His
100 105 110

336

aaa tca gat cca aag ggg gaa ttc att gtt gtt cat aat ggt att att
Lys Ser Asp Pro Lys Gly Glu Ile Val Val His Asn Gly Ile Ile
115 120 125

384

act aat tat gct gct tta aga aaa tat ctt tta tca aaa gga cat gtt
Thr Asn Tyr Ala Ala Leu Arg Lys Tyr Leu Leu Ser Lys Gly His Val
130 135 140

432

ttt gaa agt gaa act gat act gaa tgt att gct aaa tta ttt aaa cat
Phe Glu Ser Glu Thr Asp Thr Glu Cys Ile Ala Lys Leu Phe Lys His
145 150 155 160

480

ttt tat gat ttg aat gtt aaa gct ggt gtt ttc cct gat ctt aat gaa
Phe Tyr Asp Leu Asn Val Lys Ala Gly Val Phe Pro Asp Leu Asn Glu
165 170 175

528

ttg act aaa caa gtt ttg cat gaa tta gaa ggt tct tat ggg tta tta
Leu Thr Lys Gln Val Leu His Glu Leu Glu Gly Ser Tyr Gly Leu Leu
180 185 190

576

gtt aaa tct tat cat tat cct gga gaa gtt tgt ggt act aga aaa ggt
Val Lys Ser Tyr His Tyr Pro Gly Glu Val Cys Gly Thr Arg Lys Gly
195 200 205

624

tct cca tta ttg gtt ggt gtt aaa act gat aag aaa tta aaa gtt gat
Ser Pro Leu Leu Val Gly Val Lys Thr Asp Lys Lys Leu Lys Val Asp
210 215 220

672

tat tgt ttg gaa aga gga gct tta act gtt ggt atc gtt aac tct gtt Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser Val 465 470 475 480	1440
ggt tct tca atg tct aga caa acc cat tgt ggg gtt cat att aat gct Gly Ser Ser Met Ser Arg Gln Thr His Cys Gly Val His Ile Asn Ala 485 490 495	1488
ggg cca gaa att ggt gtt gcc tca act aaa gct tac aca tct caa tat Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln Tyr 500 505 510	1536
att gcc ttg gtg atg ttt gcc ctt tct tta tct aat gat tct att tcc Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asn Asp Ser Ile Ser 515 520 525	1584
aga aag gga aga cat gaa gaa att att aaa ggt tta caa aaa atc cct Arg Lys Gly Arg His Glu Glu Ile Ile Lys Gly Leu Gln Lys Ile Pro 530 535 540	1632
gaa caa att aaa caa gtt ttg aaa tta gaa aac aag atc aaa gat tta Glu Gln Ile Lys Gln Val Leu Lys Leu Glu Asn Lys Ile Lys Asp Leu 545 550 555 560	1680
tgt aat agt tca ttg aat gat caa aaa tct tta tta tta ggt aga Cys Asn Ser Ser Leu Asn Asp Gln Lys Ser Leu Leu Leu Gly Arg 565 570 575	1728
ggt tat caa ttt gct act gct tta gaa ggg gct tta aaa att aaa gaa Gly Tyr Gln Phe Ala Thr Ala Leu Glu Gly Ala Leu Lys Ile Lys Glu 580 585 590	1776
att tct tat atg cat tct gaa ggg gta tta gct ggt gaa tta aaa cat Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys His 595 600 605	1824
ggt ata tta gca tta gtc gat gaa gat tta cca att att gcc ttt gcc Gly Ile Leu Ala Leu Val Asp Glu Asp Leu Pro Ile Ile Ala Phe Ala 610 615 620	1872
act aga gat tca tta ttt cct aaa gtt atg tcc gct att gaa caa gtc Thr Arg Asp Ser Leu Phe Pro Lys Val Met Ser Ala Ile Glu Gln Val 625 630 635 640	1920
act gct aga gat ggt aga cca att gtt att tgt aat gaa ggt gat gct Thr Ala Arg Asp Gly Arg Pro Ile Val Ile Cys Asn Glu Gly Asp Ala 645 650 655	1968
att att tct aat gat aaa gtt cat act act tta gaa gtt cca gaa acc Ile Ile Ser Asn Asp Lys Val His Thr Thr Leu Glu Val Pro Glu Thr 660 665 670	2016
gtt gat tgt tta caa ggg tta aat gtt att cca tta caa ttg att Val Asp Cys Leu Gln Gly Leu Leu Asn Val Ile Pro Leu Gln Leu Ile 675 680 685	2064
agt tat tgg ttg gct gtg aat aga ggt att gat gtt gat ttc cct cgt Ser Tyr Trp Leu Ala Val Asn Arg Gly Ile Asp Val Asp Phe Pro Arg 690 695 700	2112

aac ttg gct aaa tca gtt act gtt gag taa
Asn Leu Ala Lys Ser Val Thr Val Glu
705 710

2142

<210> 20
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<213> Candida albicans

<400> 20

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Gly Glu Ile Ile Asp Asn Leu Ile Glu Gly Leu Gln Arg Leu Glu Tyr
20 25 30

Arg Gly Tyr Asp Ser Ala Gly Ile Ala Val Asp Gly Lys Leu Thr Lys
35 40 45

Asp Pro Ser Asn Gly Asp Glu Glu Tyr Met Asp Ser Ile Ile Val Lys
50 55 60

Thr Thr Gly Lys Val Lys Val Leu Lys Gln Lys Ile Ile Asp Asp Gln
65 70 75 80

Ile Asp Arg Ser Ala Ile Phe Asp Asn His Val Gly Ile Ala His Thr
85 90 95

Arg Trp Ala Thr His Gly Gln Pro Lys Thr Glu Asn Cys His Pro His
100 105 110

Lys Ser Asp Pro Lys Gly Glu Phe Ile Val Val His Asn Gly Ile Ile
115 120 125

Thr Asn Tyr Ala Ala Leu Arg Lys Tyr Leu Leu Ser Lys Gly His Val
130 135 140

Phe Glu Ser Glu Thr Asp Thr Glu Cys Ile Ala Lys Leu Phe Lys His
145 150 155 160

Phe Tyr Asp Leu Asn Val Lys Ala Gly Val Phe Pro Asp Leu Asn Glu
165 170 175

Leu Thr Lys Gln Val Leu His Glu Leu Glu Gly Ser Tyr Gly Leu Leu
180 185 190

Val Lys Ser Tyr His Tyr Pro Gly Glu Val Cys Gly Thr Arg Lys Gly
195 200 205

Ser Pro Leu Leu Val Gly Val Lys Thr Asp Lys Lys Leu Lys Val Asp
210 215 220

Phe Val Asp Val Glu Phe Glu Ala Gln Gln His Arg Pro Gln Gln
225 230 235 240

Pro Gln Ile Asn His Asn Gly Ala Thr Ser Ala Ala Glu Leu Gly Phe
245 250 255

Ile Pro Val Ala Pro Gly Glu Gln Asn Leu Arg Thr Ser Gln Ser Arg
260 265 270

Ala Phe Leu Ser Glu Asp Asp Leu Pro Met Pro Val Glu Phe Phe Leu
275 280 285

Ser Ser Asp Pro Ala Ser Val Val Gln His Thr Lys Lys Val Leu Phe
290 295 300

Leu Glu Asp Asp Asp Ile Ala His Ile Tyr Asp Gly Glu Leu Arg Ile
305 310 315 320

His Arg Ala Ser Thr Lys Ser Ala Gly Glu Ser Thr Val Arg Pro Ile
325 330 335

Gln Thr Leu Glu Met Glu Leu Asn Glu Ile Met Lys Gly Pro Tyr Lys
340 345 350

His Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Asp Ser Ala Phe Asn
355 360 365

Thr Met Arg Gly Arg Ile Asp Phe Glu Asn Cys Val Val Thr Leu Gly
370 375 380

Gly Leu Lys Ser Trp Leu Ser Thr Ile Arg Arg Cys Arg Arg Ile Ile
385 390 395 400

Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg Ser
405 410 415

Ile Phe Glu Glu Leu Thr Glu Ile Pro Val Ser Val Glu Leu Ala Ser
420 425 430

Asp Phe Leu Asp Arg Arg Ser Pro Val Phe Arg Asp Asp Thr Cys Val
435 440 445

Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Ser Ile Leu Ala Leu Gln
450 455 460

Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser Val
465 470 475 480

Gly Ser Ser Met Ser Arg Gln Thr His Cys Gly Val His Ile Asn Ala
485 490 495

Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln Tyr
500 505 510

Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asn Asp Ser Ile Ser
515 520 525

Arg Lys Gly Arg His Glu Glu Ile Ile Lys Gly Leu Gln Lys Ile Pro
530 535 540

Glu Gln Ile Lys Gln Val Leu Lys Leu Glu Asn Lys Ile Lys Asp Leu
545 550 555 560

Cys Asn Ser Ser Leu Asn Asp Gln Lys Ser Leu Leu Leu Gly Arg
565 570 575

Gly Tyr Gln Phe Ala Thr Ala Leu Glu Gly Ala Leu Lys Ile Lys Glu
580 585 590

Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys His
595 600 605

Gly Ile Leu Ala Leu Val Asp Glu Asp Leu Pro Ile Ile Ala Phe Ala
610 615 620

Thr Arg Asp Ser Leu Phe Pro Lys Val Met Ser Ala Ile Glu Gln Val
625 630 635 640

Thr Ala Arg Asp Gly Arg Pro Ile Val Ile Cys Asn Glu Gly Asp Ala
645 650 655

Ile Ile Ser Asn Asp Lys Val His Thr Thr Leu Glu Val Pro Glu Thr
660 665 670

Val Asp Cys Leu Gln Gly Leu Leu Asn Val Ile Pro Leu Gln Leu Ile
675 680 685

Ser Tyr Trp Leu Ala Val Asn Arg Gly Ile Asp Val Asp Phe Pro Arg
690 695 700

Asn Leu Ala Lys Ser Val Thr Val Glu
705 710

<210> 21
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<220>
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40

<210> 22
<211> 43
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<213> Artificial sequence

<220>
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<400> 22
gatcctcagtttactccaca gtaacactct tcgcaagggtt acg

43

<210> 23
<211> 33
<212> DNA
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<220>
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<400> 23
gatcgggtctc gcatgtgtgg tatctttgggt tac

33

<210> 24
<211> 33
<212> DNA
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<220>
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<400> 24
gatcgaattc ttatttcgacgtt gtaacagatt tag

33

<210> 25
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<400> 25
gatcggtc tc gcatgtgtgg tattttgg t acgtc 36

<210> 26
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<220>
<223> primer

<400> 26
gatcctcgag ttactcaaca gtaactgatt tagcc 35

<210> 27
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<220>
<223> primer

<400> 27
gcgggtaccc atatgtgtgg tattttgg tacgt 35

<210> 28
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<212> DNA
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<220>
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<400> 28
gcgggatcct tactcaacag taactgattt agcca 35

<210> 29
<211> 480
<212> DNA
<213> *Saccharomyces cerevisiae*

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<222> (1) .. (480)
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<400> 29

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1 5 10 15	
ttg gaa cag gtc act gag acg cta aag gtt ttg acc acc gtc ggc act	96
Leu Glu Gln Val Thr Glu Thr Leu Lys Val Leu Thr Thr Val Gly Thr	
20 25 30	
att acc ccc gaa tcc ttc agc aaa ctc ata aaa tac tgg aat gaa gcc	144
Ile Thr Pro Glu Ser Phe Ser Lys Leu Ile Lys Tyr Trp Asn Glu Ala	
35 40 45	
aca gta tgg aat gat aac gaa gat aaa aaa ata atg caa tat aac ccc	192
Thr Val Trp Asn Asp Asn Glu Asp Lys Lys Ile Met Gln Tyr Asn Pro	
50 55 60	
atg gtg att gtg gac aag cgc acc gag acg gtt gcc gct acg ggg aat	240
Met Val Ile Val Asp Lys Arg Thr Glu Thr Val Ala Ala Thr Gly Asn	
65 70 75 80	
atc atc atc gaa aga aag atc att cat gaa ctg ggg cta tgt ggc cac	288
Ile Ile Ile Glu Arg Lys Ile Ile His Glu Leu Gly Leu Cys Gly His	
85 90 95	
atc gag gac att gca gta aac tcc aag tat cag ggc caa ggt ttg ggc	336
Ile Glu Asp Ile Ala Val Asn Ser Lys Tyr Gln Gly Gln Gly Leu Gly	
100 105 110	
aag ctc ttg att gat caa ttg gta act atc ggc ttt gac tac ggt tgt	384
Lys Leu Ile Asp Gln Leu Val Thr Ile Gly Phe Asp Tyr Gly Cys	
115 120 125	
tat aag att att tta gat tgc gat gag aaa aat gtc aaa ttc tat gaa	432
Tyr Lys Ile Ile Leu Asp Cys Asp Glu Lys Asn Val Lys Phe Tyr Glu	
130 135 140	
aaa tgt ggg ttt agc aac gca ggc gtg gaa atg caa att aga aaa tag	480
Lys Cys Gly Phe Ser Asn Ala Gly Val Glu Met Gln Ile Arg Lys	
145 150 155	
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<400> 30	
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Leu Glu Gln Val Thr Glu Thr Leu Lys Val Leu Thr Thr Val Gly Thr	
20 25 30	
Ile Thr Pro Glu Ser Phe Ser Lys Leu Ile Lys Tyr Trp Asn Glu Ala	
35 40 45	

Thr Val Trp Asn Asp Asn Glu Asp Lys Lys Ile Met Gln Tyr Asn Pro
50 55 60

Met Val Ile Val Asp Lys Arg Thr Glu Thr Val Ala Ala Thr Gly Asn
65 70 75 80

Ile Ile Ile Glu Arg Lys Ile Ile His Glu Leu Gly Leu Cys Gly His
85 90 95

Ile Glu Asp Ile Ala Val Asn Ser Lys Tyr Gln Gly Gln Gly Leu Gly
100 105 110

Lys Leu Leu Ile Asp Gln Leu Val Thr Ile Gly Phe Asp Tyr Gly Cys
115 120 125

Tyr Lys Ile Ile Leu Asp Cys Asp Glu Lys Asn Val Lys Phe Tyr Glu
130 135 140

Lys Cys Gly Phe Ser Asn Ile Gly Val Glu Met Gln Ile Arg Lys
145 150 155

<210> 31
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<212> DNA
<213> Candida albicans

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1 5 10 15

tat gat aat caa tat tta gaa act tta aaa gtt ttg acg aca gtt ggt 96
Tyr Asp Asn Gln Tyr Leu Glu Thr Leu Lys Val Leu Thr Thr Val Gly
20 25 30

gaa att tcc aaa gaa gat ttc act gaa ttg tat aat cat tgg tct tca 144
Glu Ile Ser Lys Glu Asp Phe Thr Glu Leu Tyr Asn His Trp Ser Ser
35 40 45

ttg cca tct att tat cat cca tat gta atc acc aat gca tca ggt ata 192
Leu Pro Ser Ile Tyr His Pro Tyr Val Ile Thr Asn Ala Ser Gly Ile
50 55 60

gtg gta gcc acg ggg atg tta ttt gtg gag aaa aaa ttg att cat gaa 240
Val Val Ala Thr Gly Met Leu Phe Val Glu Lys Lys Leu Ile His Glu
65 70 75 80

tgt ggt aaa gtt ggt cat att gaa gat att tca gtt gct aaa tct gaa	288
Cys Gly Lys Val Gly His Ile Glu Asp Ile Ser Val Ala Lys Ser Glu	
85 90 95	
caa ggt aaa aaa ttg gga tat tat tta gtc act tca tta acc aaa gtt	336
Gln Gly Lys Lys Leu Gly Tyr Tyr Leu Val Thr Ser Leu Thr Lys Val	
100 105 110	
gct caa gag aat gat tgt tac aaa gtc att tta gat tgt tct cct gaa	384
Ala Gln Glu Asn Asp Cys Tyr Lys Val Ile Leu Asp Cys Ser Pro Glu	
115 120 125	
aat gtt ggc ttt tat gaa aaa tgt ggt tat aaa gat ggt ggt gtt gaa	432
Asn Val Gly Phe Tyr Glu Lys Cys Gly Tyr Lys Asp Gly Gly Val Glu	
130 135 140	
atg gta tgt aga ttc tag	450
Met Val Cys Arg Phe	
145	
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Tyr Asp Asn Gln Tyr Leu Glu Thr Leu Lys Val Leu Thr Thr Val Gly	
20 25 30	
Glu Ile Ser Lys Glu Asp Phe Thr Glu Leu Tyr Asn His Trp Ser Ser	
35 40 45	
Leu Pro Ser Ile Tyr His Pro Tyr Val Ile Thr Asn Ala Ser Gly Ile	
50 55 60	
Val Val Ala Thr Gly Met Leu Phe Val Glu Lys Lys Leu Ile His Glu	
65 70 75 80	
Cys Gly Lys Val Gly His Ile Glu Asp Ile Ser Val Ala Lys Ser Glu	
85 90 95	
Gln Gly Lys Lys Leu Gly Tyr Tyr Leu Val Thr Ser Leu Thr Lys Val	
100 105 110	
Ala Gln Glu Asn Asp Cys Tyr Lys Val Ile Leu Asp Cys Ser Pro Glu	
115 120 125	

Asn Val Gly Phe Tyr Glu Lys Cys Gly Tyr Lys Asp Gly Gly Val Glu
130 135 140

Met Val Cys Arg Phe
145

<210> 33
<211> 450
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(450)
<223>

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Met Ala Glu Thr Phe Lys Ile Arg Lys Leu Glu Ile Ser Asp Lys Arg
1 5 10 15

aaa gga ttc atc gag ctt cta ggt caa cta acc gtc acc gga tca gta
Lys Gly Phe Ile Glu Leu Leu Gly Gln Leu Thr Val Thr Gly Ser Val
20 25 30

aca gac gaa gaa ttc gat cgg cga ttc gaa gaa atc aga tcg tat ggt
Thr Asp Glu Glu Phe Asp Arg Arg Phe Glu Glu Ile Arg Ser Tyr Gly
35 40 45

gac gac cac gtg atc tgc gtg atc gaa gaa act tcg gga aaa atc
Asp Asp His Val Ile Cys Val Ile Glu Glu Thr Ser Gly Lys Ile
50 55 60

gct gct acg ggt agt gtg atg ata gag aag aag ttt ctg agg aat tgc
Ala Ala Thr Gly Ser Val Met Ile Glu Lys Lys Phe Leu Arg Asn Cys
65 70 75 80

ggt aaa gct ggg cac att gaa gac gtt gtt gtg gat tca agg ttt cgc
Gly Lys Ala Gly His Ile Glu Asp Val Val Asp Ser Arg Phe Arg
85 90 95

ggg aaa cag ctg ggg aag aaa gtt gtt gag ttt ctt atg gat cat tgc
Gly Lys Gln Leu Gly Lys Val Val Glu Phe Leu Met Asp His Cys
100 105 110

aaa tca atg ggt tgc tat aag gtg att cta gat tgt agt gtg gag aac
Lys Ser Met Gly Cys Tyr Lys Val Ile Leu Asp Cys Ser Val Glu Asn
115 120 125

aaa gtg ttc tat gag aaa tgt ggg atg agt aat aaa tcg att caa atg
Lys Val Phe Tyr Glu Lys Cys Gly Met Ser Asn Lys Ser Ile Gln Met
130 135 140

tct aag tac ttc gat taa
Ser Lys Tyr Phe Asp
145

<210> 34
<211> 149
<212> PRT
<213> Arabidopsis thaliana

<400> 34

Met Ala Glu Thr Phe Lys Ile Arg Lys Leu Glu Ile Ser Asp Lys Arg
1 5 10 15

Lys Gly Phe Ile Glu Leu Leu Gly Gln Leu Thr Val Thr Gly Ser Val
20 25 30

Thr Asp Glu Glu Phe Asp Arg Arg Phe Glu Glu Ile Arg Ser Tyr Gly
35 40 45

Asp Asp His Val Ile Cys Val Ile Glu Glu Glu Thr Ser Gly Lys Ile
50 55 60

Ala Ala Thr Gly Ser Val Met Ile Glu Lys Lys Phe Leu Arg Asn Cys
65 70 75 80

Gly Lys Ala Gly His Ile Glu Asp Val Val Val Asp Ser Arg Phe Arg
85 90 95

Gly Lys Gln Leu Gly Lys Lys Val Val Glu Phe Leu Met Asp His Cys
100 105 110

Lys Ser Met Gly Cys Tyr Lys Val Ile Leu Asp Cys Ser Val Glu Asn
115 120 125

Lys Val Phe Tyr Glu Lys Cys Gly Met Ser Asn Lys Ser Ile Gln Met
130 135 140

Ser Lys Tyr Phe Asp
145

<210> 35
<211> 43
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 35
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43

<210> 36
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 36
gatcctcgag ctatttctta atttgcattt ccacgcctgc 40

<210> 37
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 37
gatcggtctc gcatgatgtt accacaaggt tatac 35

<210> 38
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 38
gatcctcgag ctagaatcta cataccattt caac 34

<210> 39
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 39
gatggctctcg catggctgag acattcaaga tc 32

<210> 40
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 40
gatcctcgag ttaatcgaag tacttagaca tttgaatc 38

<210> 41
<211> 801
<212> DNA
<213> Escherichia coli

<220>
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<222> (1) .. (801)
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Met Arg Leu Ile Pro Leu Thr Thr Ala Glu Gln Val Gly Lys Trp Ala
1 5 10 15
gct cgc cat atc gtc aat cgt atc aat gcg ttc aaa ccg act gcc gat 96
Ala Arg His Ile Val Asn Arg Ile Asn Ala Phe Lys Pro Thr Ala Asp
20 25 30
cgt ccg ttt gta ctg ggc ctg ccg act ggc ggc acg ccg atg acc acc 144
Arg Pro Phe Val Leu Gly Leu Pro Thr Gly Thr Pro Met Thr Thr
35 40 45
tat aaa gcg tta gtc gaa atg cat aaa gca ggc cag gtc agc ttt aag 192
Tyr Lys Ala Leu Val Glu Met His Lys Ala Gly Gln Val Ser Phe Lys
50 55 60
cac gtt gtc acc ttc aac atg gac gaa tat gtc ggt ctg ccg aaa gag 240
His Val Val Thr Phe Asn Met Asp Glu Tyr Val Gly Leu Pro Lys Glu
65 70 75 80
cat ccg gaa agc tac tac agc ttt atg cac cgt aat ttc ttc gat cac 288
His Pro Glu Ser Tyr Tyr Ser Phe Met His Arg Asn Phe Asp His
85 90 95
gtt gat att cca gca gaa aac atc aac ctt ctc aac ggc aac gcc ccg 336
Val Asp Ile Pro Ala Glu Asn Ile Asn Leu Leu Asn Gly Asn Ala Pro
100 105 110
gat atc gac gcc gag tgc cgc cag tat gaa gaa aaa atc cgt tct tac 384
Asp Ile Asp Ala Glu Cys Arg Gln Tyr Glu Glu Lys Ile Arg Ser Tyr
115 120 125
gga aaa att cat ctg ttt atg ggc ggt gta ggt aac gac ggt cat att 432
Gly Lys Ile His Leu Phe Met Gly Gly Val Gly Asn Asp Gly His Ile
130 135 140
gca ttt aac gaa ccg gcg tct tct ctg gct tct cgt act cgt atc aaa 480
Ala Phe Asn Glu Pro Ala Ser Ser Leu Ala Ser Arg Thr Arg Ile Lys
145 150 155 160
acc ctg act cat gac act cgc gtc gca aac tct cgt ttc ttt gat aac 528
Thr Leu Thr His Asp Thr Arg Val Ala Asn Ser Arg Phe Phe Asp Asn
165 170 175
gat gtt aat cag gtg cca aaa tat gcc ctg act gtc ggt gtt ggt aca 576
Asp Val Asn Gln Val Pro Lys Tyr Ala Leu Thr Val Gly Val Gly Thr
180 185 190

ctg ctg gat gcc gaa gaa gtg atg att ctg gtg ctg ggt agc cag aaa Leu Leu Asp Ala Glu Glu Val Met Ile Leu Val Leu Gly Ser Gln Lys 195 200 205	624
gca ctg gcg ctg cag gcc gtt gaa ggt tgc gtg aac cat atg tgg Ala Leu Ala Leu Gln Ala Ala Val Glu Gly Cys Val Asn His Met Trp 210 215 220	672
acc atc agc tgt ctg caa ctg cat ccg aaa gcg atc atg gtg tgc gat Thr Ile Ser Cys Leu Gln Leu His Pro Lys Ala Ile Met Val Cys Asp 225 230 235 240	720
gaa cct tcc acc atg gag ctg aaa gtt aag act tta aga tat ttc aat Glu Pro Ser Thr Met Glu Leu Lys Val Lys Thr Leu Arg Tyr Phe Asn 245 250 255	768
gaa tta gaa gca gaa aat atc aaa ggt ctg taa Glu Leu Glu Ala Glu Asn Ile Lys Gly Leu 260 265	801
<p><210> 42 <211> 266 <212> PRT <213> Escherichia coli</p> <p><400> 42</p>	
Met Arg Leu Ile Pro Leu Thr Thr Ala Glu Gln Val Gly Lys Trp Ala 1 5 10 15	
Ala Arg His Ile Val Asn Arg Ile Asn Ala Phe Lys Pro Thr Ala Asp 20 25 30	
Arg Pro Phe Val Leu Gly Leu Pro Thr Gly Gly Thr Pro Met Thr Thr 35 40 45	
Tyr Lys Ala Leu Val Glu Met His Lys Ala Gly Gln Val Ser Phe Lys 50 55 60	
His Val Val Thr Phe Asn Met Asp Glu Tyr Val Gly Leu Pro Lys Glu 65 70 75 80	
His Pro Glu Ser Tyr Tyr Ser Phe Met His Arg Asn Phe Phe Asp His 85 90 95	
Val Asp Ile Pro Ala Glu Asn Ile Asn Leu Leu Asn Gly Asn Ala Pro 100 105 110	
Asp Ile Asp Ala Glu Cys Arg Gln Tyr Glu Glu Lys Ile Arg Ser Tyr 115 120 125	

Gly Lys Ile His Leu Phe Met Gly Gly Val Gly Asn Asp Gly His Ile
130 135 140

Ala Phe Asn Glu Pro Ala Ser Ser Leu Ala Ser Arg Thr Arg Ile Lys
145 150 155 160

Thr Leu-Thr His Asp Thr Arg Val Ala Asn Ser Arg Phe Phe Asp Asn
165 170 175

Asp Val Asn Gln Val Pro Lys Tyr Ala Leu Thr Val Gly Val Gly Thr
180 185 190

Leu Leu Asp Ala Glu Glu Val Met Ile Leu Val Leu Gly Ser Gln Lys
195 200 205

Ala Leu Ala Leu Gln Ala Ala Val Glu Gly Cys Val Asn His Met Trp
210 215 220

Thr Ile Ser Cys Leu Gln Leu His Pro Lys Ala Ile Met Val Cys Asp
225 230 235 240

Glu Pro Ser Thr Met Glu Leu Lys Val Lys Thr Leu Arg Tyr Phe Asn
245 250 255

Glu Leu Glu Ala Glu Asn Ile Lys Gly Leu
260 265

<210> 43
<211> 31
<212> DNA
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<220>
<223> primer

<400> 43
gatggtctcg catgagactg atccccctga c

31

<210> 44
<211> 43
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43

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<211> 32	
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gatcctgcag tcatgctgct aataatctat cc	32
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gatctacgta agcaaccgca cctgtggc	28
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<211> 36	
<212> DNA	
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gatccaattg atccggatat agttcctcct ttcagc	36
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<212> DNA	
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<210> 50
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<212> DNA
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<400> 50
gatcgtcgac ttagtacagc ggcttaccgc tactgtc 37

<210> 51
<211> 35
<212> DNA
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<220>
<223> primer

<400> 51
gatgcggccg catggcaatg acttaccacc tggac 35

<210> 52
<211> 29
<212> DNA
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<220>
<223> primer

<400> 52
cgtaccaggc tgctctgcct gaagcaccc 29

<210> 53
<211> 1338
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1338)
<223>

<400> 53
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Met Ser Asn Arg Lys Tyr Phe Gly Thr Asp Gly Ile Arg Gly Arg Val
1 5 10 15

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Gly Asp Ala Pro Ile Thr Pro Asp Phe Val Leu Lys Leu Gly Trp Ala
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gct ggt aaa gtg ctg gct cgc cac ggc tcc cgt aag att att att ggt
Ala Gly Lys Val Leu Ala Arg His Gly Ser Arg Lys Ile Ile Ile Gly
35 40 45 144

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aaa gac acg cgt att tct ggc tat atg ctg gag tca gca ctg gaa gcg Lys Asp Thr Arg Ile Ser Gly Tyr Met Leu Glu Ser Ala Leu Glu Ala 50 55 60	192
ggt ctg gcg gca gcg ggc ctt tcc gca ctc ttc act ggc ccg atg cca Gly Leu Ala Ala Ala Gly Leu Ser Ala Leu Phe Thr Gly Pro Met Pro 65 70 75 80	240
aca ccg gcc gtg gct tat ctg acg cgt acc ttc cgc gca gag gcc gga Thr Pro Ala Val Ala Tyr Leu Thr Arg Thr Phe Arg Ala Glu Ala Gly 85 90 95	288
att gtg ata tct gca tcg cat aac ccg ttc tac gat aat ggc att aaa Ile Val Ile Ser Ala Ser His Asn Pro Phe Tyr Asp Asn Gly Ile Lys 100 105 110	336
ttc ttc tct atc gac ggc acc aaa ctg ccg gat gcg gta gaa gag gcc Phe Phe Ser Ile Asp Gly Thr Lys Leu Pro Asp Ala Val Glu Glu Ala 115 120 125	384
atc gaa gcg gaa atg gaa aag gag atc agc tgc gtt gat tcg gca gaa Ile Glu Ala Glu Met Glu Lys Glu Ile Ser Cys Val Asp Ser Ala Glu 130 135 140	432
ctg ggt aaa gcc agc cgt atc gtt gat gcc gcg ggt cgc tat atc gag Leu Gly Lys Ala Ser Arg Ile Val Asp Ala Ala Gly Arg Tyr Ile Glu 145 150 155 160	480
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gtg ctg cgc gaa ctg ggg gcg aac gtt atc gct atc ggt tgt gag cca Val Leu Arg Glu Leu Gly Ala Asn Val Ile Ala Ile Gly Cys Glu Pro 195 200 205	624
aac ggt gta aac atc aat gcc gaa gtg ggg gct acc gac gtt cgc gcg Asn Gly Val Asn Ile Asn Ala Glu Val Gly Ala Thr Asp Val Arg Ala 210 215 220	672
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cag ggc cag ctg cgt ggt ggc gct gtg ggt aca ttg atg agc aac atg Gln Gly Gln Leu Arg Gly Gly Ala Val Gly Thr Leu Met Ser Asn Met 275 280 285	864

ggg ctt gaa ctg gcg ctg aaa cag tta gga att cca ttt gcg cgc gcg	912
Gly Leu Glu Leu Ala Leu Lys Gln Leu Gly Ile Pro Phe Ala Arg Ala	
290 295 300	
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Lys Val Gly Asp Arg Tyr Val Leu Glu Lys Met Gln Glu Lys Gly Trp	
305 310 315 320	
cgt atc ggt gca gag aat tcc ggt cat gtg atc ctg ctg gat aaa act	1008
Arg Ile Gly Ala Glu Asn Ser Gly His Val Ile Leu Leu Asp Lys Thr	
325 330 335	
act acc ggt gac ggc atc gtt gct ggc ttg cag gtg ctg gcg gcg atg	1056
Thr Thr Gly Asp Gly Ile Val Ala Gly Leu Gln Val Leu Ala Ala Met	
340 345 350	
gca cgt aac cat atg agc ctg cac gac ctt tgc agc ggc atg aaa atg	1104
Ala Arg Asn His Met Ser Leu His Asp Leu Cys Ser Gly Met Lys Met	
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ttc ccg cag att ctg gtt aac gta cgt tac acc gca ggt agc ggc gat	1152
Phe Pro Gln Ile Leu Val Asn Val Arg Tyr Thr Ala Gly Ser Gly Asp	
370 375 380	
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Pro Leu Glu His Glu Ser Val Lys Ala Val Thr Ala Glu Val Glu Ala	
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Ala Leu Gly Asn Arg Gly Arg Val Leu Leu Arg Lys Ser Gly Thr Glu	
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Pro Leu Ile Arg Val Met Val Glu Gly Glu Asp Glu Ala Gln Val Thr	
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35 40 45	

Lys Asp Thr Arg Ile Ser Gly Tyr Met Leu Glu Ser Ala Leu Glu Ala
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Gly Leu Ala Ala Ala Gly Leu Ser Ala Leu Phe Thr Gly Pro Met Pro
65 70 75 80

Thr Pro Ala Val Ala Tyr Leu Thr Arg Thr Phe Arg Ala Glu Ala Gly
85 90 95

Ile Val Ile Ser Ala Ser His Asn Pro Phe Tyr Asp Asn Gly Ile Lys
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Phe Phe Ser Ile Asp Gly Thr Lys Leu Pro Asp Ala Val Glu Glu Ala
115 120 125

Ile Glu Ala Glu Met Glu Lys Glu Ile Ser Cys Val Asp Ser Ala Glu
130 135 140

Leu Gly Lys Ala Ser Arg Ile Val Asp Ala Ala Gly Arg Tyr Ile Glu
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165 170 175

Ile Val Val Asp Cys Ala Asn Gly Ala Thr Tyr His Ile Ala Pro Asn
180 185 190

Val Leu Arg Glu Leu Gly Ala Asn Val Ile Ala Ile Gly Cys Glu Pro
195 200 205

Asn Gly Val Asn Ile Asn Ala Glu Val Gly Ala Thr Asp Val Arg Ala
210 215 220

Leu Gln Ala Arg Val Leu Ala Glu Lys Ala Asp Leu Gly Ile Ala Phe
225 230 235 240

Asp Gly Asp Gly Asp Arg Val Ile Met Val Asp His Glu Gly Asn Lys
245 250 255

Val Asp Gly Asp Gln Ile Met Tyr Ile Ile Ala Arg Glu Gly Leu Arg
260 265 270

Gln Gly Gln Leu Arg Gly Gly Ala Val Gly Thr Leu Met Ser Asn Met
275 280 285

Gly Leu Glu Leu Ala Leu Lys Gln Leu Gly Ile Pro Phe Ala Arg Ala
290 295 300

Lys Val Gly Asp Arg Tyr Val Leu Glu Lys Met Gln Glu Lys Gly Trp
305 310 315 320

Arg Ile Gly Ala Glu Asn Ser Gly His Val Ile Leu Leu Asp Lys Thr
325 330 335

Thr Thr Gly Asp Gly Ile Val Ala Gly Leu Gln Val Leu Ala Ala Met
340 345 350

Ala Arg Asn His Met Ser Leu His Asp Leu Cys Ser Gly Met Lys Met
355 360 365

Phe Pro Gln Ile Leu Val Asn Val Arg Tyr Thr Ala Gly Ser Gly Asp
370 375 380

Pro Leu Glu His Glu Ser Val Lys Ala Val Thr Ala Glu Val Glu Ala
385 390 395 400

Ala Leu Gly Asn Arg Gly Arg Val Leu Leu Arg Lys Ser Gly Thr Glu
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acg cgc atg tat tcc gat ctt ccg aaa gtg ctg cat acc ctt gcc ggg 96
Thr Arg Met Tyr Ser Asp Leu Pro Lys Val Leu His Thr Leu Ala Gly
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aaa gcg atg gtt cag cat gtc att gat gct gcg aat gaa tta ggc gca	144
Lys Ala Met Val Gln His Val Ile Asp Ala Ala Asn Glu Leu Gly Ala	
35 40 45	
gcg cac gtt cac ctg gtg tac ggt cac ggc ggc gat ctg cta aaa cag	192
Ala His Val His Leu Val Tyr Gly His Gly Gly Asp Leu Leu Lys Gln	
50 55 60	
gcg ctg aaa gac gac aac ctt aac tgg gtg ctt cag gca gag cag ctg	240
Ala Leu Lys Asp Asp Asn Leu Asn Trp Val Leu Gln Ala Glu Gln Leu	
65 70 75 80	
ggt acg ggt cat gca atg cag cag gcc gca cct ttc ttt gcc gat gat	288
Gly Thr Gly His Ala Met Gln Gln Ala Ala Pro Phe Phe Ala Asp Asp	
85 90 95	
gaa gac att tta atg ctc tac ggc gac gtg ccg ctg atc tct gtc gaa	336
Glu Asp Ile Met Leu Tyr Gly Asp Val Pro Leu Ile Ser Val Glu	
100 105 110	
aca ctc cag cgt ctg cgt gat gct aaa ccg cag ggt ggc att ggt ctg	384
Thr Leu Gln Arg Leu Arg Asp Ala Lys Pro Gln Gly Gly Ile Gly Leu	
115 120 125	
ctg acg gtg aaa ctg gat gat ccg acc ggt tat gga cgt atc acc cgt	432
Leu Thr Val Lys Leu Asp Asp Pro Thr Gly Tyr Gly Arg Ile Thr Arg	
130 135 140	
gaa aac ggc aaa gtt acc ggc att gtt gag cac aaa gat gcc acc gac	480
Glu Asn Gly Lys Val Thr Gly Ile Val Glu His Lys Asp Ala Thr Asp	
145 150 155 160	
gag cag cgt cag att cag gag atc aac acc ggc att ctg att gcc aac	528
Glu Gln Arg Gln Ile Gln Glu Ile Asn Thr Gly Ile Leu Ile Ala Asn	
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Gly Ala Asp Met Lys Arg Trp Leu Ala Lys Leu Thr Asn Asn Asn Ala	
180 185 190	
cag ggc gaa tac tac atc acc gac att att gcg ctg gcg tat cag gaa	624
Gln Gly Glu Tyr Tyr Ile Thr Asp Ile Ile Ala Leu Ala Tyr Gln Glu	
195 200 205	
ggg cgt gaa atc gtc gcc gtt cat ccg caa cgt tta agc gaa gta gaa	672
Gly Arg Glu Ile Val Ala Val His Pro Gln Arg Leu Ser Glu Val Glu	
210 215 220	
ggc gtg aat aac cgc ctg caa ctc tcc cgt ctg gag cgt gtt tat cag	720
Gly Val Asn Asn Arg Leu Gln Leu Ser Arg Leu Glu Arg Val Tyr Gln	
225 230 235 240	
tcc gaa cag gct gaa aaa ctg ctg tta gca ggc gtt atg ctg cgc gat	768
Ser Glu Gln Ala Glu Lys Leu Leu Ala Gly Val Met Leu Arg Asp	
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cca gcg cgt ttt gat ctg cgt ggt acg cta act cac ggg cgc gat gtt	816
Pro Ala Arg Phe Asp Leu Arg Gly Thr Leu Thr His Gly Arg Asp Val	
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Glu Ile Asp Thr Asn Val Ile Ile Glu Gly Asn Val Thr Leu Gly His	
275 280 285	
cgc gtg aaa att ggc acc ggt tgc gtg att aaa aac agc gtg att ggc	912
Arg Val Lys Ile Gly Thr Gly Cys Val Ile Lys Asn Ser Val Ile Gly	
290 295 300	
gat gat tgc gaa atc agt ccg tat acc gtt gtg gaa gat gcg aat ctg	960
Asp Asp Cys Glu Ile Ser Pro Tyr Thr Val Val Glu Asp Ala Asn Leu	
305 310 315 320	
gca gcg gcc tgc acc att ggc ccg ttt gcc cgt ttg cgt cct ggt gct	1008
Ala Ala Ala Cys Thr Ile Gly Pro Phe Ala Arg Leu Arg Pro Gly Ala	
325 330 335	
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Ala Arg Leu Gly Lys Gly Ser Lys Ala Gly His Leu Thr Tyr Leu Gly	
355 360 365	
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Asp Ala Glu Ile Gly Asp Asn Val Asn Ile Gly Ala Gly Thr Ile Thr	
370 375 380	
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Cys Asn Tyr Asp Gly Ala Asn Lys Phe Lys Thr Ile Ile Gly Asp Asp	
385 390 395 400	
gtg ttt gtt ggt tcc gac act cag ctg gtg gcc ccg gta aca gta ggc	1248
Val Phe Val Gly Ser Asp Thr Gln Leu Val Ala Pro Val Thr Val Gly	
405 410 415	
aaa ggc gcg acc att gct gcg ggt aca act gtg acg cgt aat gtc ggc	1296
Lys Gly Ala Thr Ile Ala Ala Gly Thr Thr Val Thr Arg Asn Val Gly	
420 425 430	
gaa aat gca tta gct atc agc cgt gtg ccg cag act cag aaa gaa ggc	1344
Glu Asn Ala Leu Ala Ile Ser Arg Val Pro Gln Thr Gln Lys Glu Gly	
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35 40 45

Ala His Val His Leu Val Tyr Gly His Gly Gly Asp Leu Leu Lys Gln
50 55 60

Ala Leu Lys Asp Asp Asn Leu Asn Trp Val Leu Gln Ala Glu Gln Leu
65 70 75 80

Gly Thr Gly His Ala Met Gln Gln Ala Ala Pro Phe Phe Ala Asp Asp
85 90 95

Glu Asp Ile Leu Met Leu Tyr Gly Asp Val Pro Leu Ile Ser Val Glu
100 105 110

Thr Leu Gln Arg Leu Arg Asp Ala Lys Pro Gln Gly Gly Ile Gly Leu
115 120 125

Leu Thr Val Lys Leu Asp Asp Pro Thr Gly Tyr Gly Arg Ile Thr Arg
130 135 140

Glu Asn Gly Lys Val Thr Gly Ile Val Glu His Lys Asp Ala Thr Asp
145 150 155 160

Glu Gln Arg Gln Ile Gln Glu Ile Asn Thr Gly Ile Leu Ile Ala Asn
165 170 175

Gly Ala Asp Met Lys Arg Trp Leu Ala Lys Leu Thr Asn Asn Asn Ala
180 185 190

Gln Gly Glu Tyr Tyr Ile Thr Asp Ile Ile Ala Leu Ala Tyr Gln Glu
195 200 205

Gly Arg Glu Ile Val Ala Val His Pro Gln Arg Leu Ser Glu Val Glu
210 215 220

Gly Val Asn Asn Arg Leu Gln Leu Ser Arg Leu Glu Arg Val Tyr Gln
225 230 235 240

Ser Glu Gln Ala Glu Lys Leu Leu Ala Gly Val Met Leu Arg Asp
245 250 255

Pro Ala Arg Phe Asp Leu Arg Gly Thr Leu Thr His Gly Arg Asp Val
260 265 270

Glu Ile Asp Thr Asn Val Ile Ile Glu Gly Asn Val Thr Leu Gly His
275 280 285

Arg Val Lys Ile Gly Thr Gly Cys Val Ile Lys Asn Ser Val Ile Gly
290 295 300

Asp Asp Cys Glu Ile Ser Pro Tyr Thr Val Val Glu Asp Ala Asn Leu
305 310 315 320

Ala Ala Ala Cys Thr Ile Gly Pro Phe Ala Arg Leu Arg Pro Gly Ala
325 330 335

Glu Leu Leu Glu Gly Ala His Val Gly Asn Phe Val Glu Met Lys Lys
340 345 350

Ala Arg Leu Gly Lys Gly Ser Lys Ala Gly His Leu Thr Tyr Leu Gly
355 360 365

Asp Ala Glu Ile Gly Asp Asn Val Asn Ile Gly Ala Gly Thr Ile Thr
370 375 380

Cys Asn Tyr Asp Gly Ala Asn Lys Phe Lys Thr Ile Ile Gly Asp Asp
385 390 395 400

Val Phe Val Gly Ser Asp Thr Gln Leu Val Ala Pro Val Thr Val Gly
405 410 415

Lys Gly Ala Thr Ile Ala Ala Gly Thr Thr Val Thr Arg Asn Val Gly
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Phe Ala Asp Asp Glu Asp Ile Leu Met Leu Tyr Gly Asp Val Pro Leu	
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atc tct gtc gaa aca ctc cag cgt ctg cgt gat gct aaa ccg cag ggt	144
Ile Ser Val Glu Thr Leu Gln Arg Leu Arg Asp Ala Lys Pro Gln Gly	
35 40 45	
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Gly Ile Gly Leu Leu Thr Val Lys Leu Asp Asp Pro Thr Gly Tyr Gly	
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Arg Ile Thr Arg Glu Asn Gly Lys Val Thr Gly Ile Val Glu His Lys	
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Asp Ala Thr Asp Glu Gln Arg Gln Ile Gln Glu Ile Asn Thr Gly Ile	
85 90 95	
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Leu Ile Ala Asn Gly Ala Asp Met Lys Arg Trp Leu Ala Lys Leu Thr	
100 105 110	
aac aat aat gct cag ggc gaa tac tac atc acc gac att att gcg ctg	384
Asn Asn Asn Ala Gln Gly Glu Tyr Tyr Ile Thr Asp Ile Ile Ala Leu	
115 120 125	
gcg tat cag gaa ggg cgt gaa atc gtc gcc gtt cat ccg caa cgt tta	432
Ala Tyr Gln Glu Gly Arg Glu Ile Val Ala Val His Pro Gln Arg Leu	
130 135 140	
agc gaa gta gaa ggc gtg aat aac cgc ctg caa ctc tcc cgt ctg gag	480
Ser Glu Val Glu Gly Val Asn Asn Arg Leu Gln Leu Ser Arg Leu Glu	
145 150 155 160	
cgt gtt tat cag tcc gaa cag gct gaa aaa ctg ctg tta gca ggc gtt	528
Arg Val Tyr Gln Ser Glu Gln Ala Glu Lys Leu Leu Leu Ala Gly Val	
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Met Leu Arg Asp Pro Ala Arg Phe Asp Leu Arg Gly Thr Leu Thr His	
180 185 190	
ggg cgc gat gtt gaa att gat act aac gtt atc atc gag ggc aac gtg	624
Gly Arg Asp Val Glu Ile Asp Thr Asn Val Ile Ile Glu Gly Asn Val	
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Thr Leu Gly His Arg Val Lys Ile Gly Thr Gly Cys Val Ile Lys Asn	
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gag atg aaa aaa gcg cgt ctg ggt aaa ggc tcg aaa gct ggt cat ctg Glu Met Lys Lys Ala Arg Leu Gly Lys Ser Lys Ala Gly His Leu 275 280 285	864
act tac ctg ggc gat gcg gaa att ggc gat aac gtt aac atc ggc gcg Thr Tyr Leu Gly Asp Ala Glu Ile Gly Asp Asn Val Asn Ile Gly Ala 290 295 300	912
gga acc att acc tgc aac tac gat ggt gcg aat aaa ttt aag acc att Gly Thr Ile Thr Cys Asn Tyr Asp Gly Ala Asn Lys Phe Lys Thr Ile 305 310 315 320	960
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gta aca gta ggc aaa ggc gcg acc att gct gcg ggt aca act gtg acg Val Thr Val Gly Lys Gly Ala Thr Ile Ala Ala Gly Thr Thr Val Thr 340 345 350	1056
cgt aat gtc ggc gaa aat gca tta gct atc agc cgt gtg ccg cag act Arg Asn Val Gly Glu Asn Ala Leu Ala Ile Ser Arg Val Pro Gln Thr 355 360 365	1104
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 35 40 45

Gly Ile Gly Leu Leu Thr Val Lys Leu Asp Asp Pro Thr Gly Tyr Gly

50 55 60

Arg Ile Thr Arg Glu Asn Gly Lys Val Thr Gly Ile Val Glu His Lys

65 70 75 80

Asp Ala Thr Asp Glu Gln Arg Gln Ile Gln Glu Ile Asn Thr Gly Ile

85 90 95

Leu Ile Ala Asn Gly Ala Asp Met Lys Arg Trp Leu Ala Lys Leu Thr

100 105 110

Asn Asn Asn Ala Gln Gly Glu Tyr Tyr Ile Thr Asp Ile Ile Ala Leu

115 120 125

Ala Tyr Gln Glu Gly Arg Glu Ile Val Ala Val His Pro Gln Arg Leu

130 135 140

Ser Glu Val Glu Gly Val Asn Asn Arg Leu Gln Leu Ser Arg Leu Glu

145 150 155 160

Arg Val Tyr Gln Ser Glu Gln Ala Glu Lys Leu Leu Leu Ala Gly Val

165 170 175

Met Leu Arg Asp Pro Ala Arg Phe Asp Leu Arg Gly Thr Leu Thr His

180 185 190

Gly Arg Asp Val Glu Ile Asp Thr Asn Val Ile Ile Glu Gly Asn Val

195 200 205

Thr Leu Gly His Arg Val Lys Ile Gly Thr Gly Cys Val Ile Lys Asn

210 215 220

Ser Val Ile Gly Asp Asp Cys Glu Ile Ser Pro Tyr Thr Val Val Glu

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260 265 270

Glu Met Lys Lys Ala Arg Leu Gly Lys Gly Ser Lys Ala Gly His Leu

275 280 285

Thr Tyr Leu Gly Asp Ala Glu Ile Gly Asp Asn Val Asn Ile Gly Ala
290 295 300

Gly Thr Ile Thr Cys Asn Tyr Asp Gly Ala Asn Lys Phe Lys Thr Ile
305 310 315 320

Ile Gly Asp Asp Val Phe Val Gly Ser Asp Thr Gln Leu Val Ala Pro
325 330 335

Val Thr Val Gly Lys Gly Ala Thr Ile Ala Ala Gly Thr Thr Val Thr
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Gln Lys Glu Gly Trp Arg Arg Pro Val Lys Lys Lys
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gatccctcgag tcacttttc tttaccggac gac 33

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<210> 72
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<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 72
gatctgtaca agcaaccgca cctgtggc

28

<210> 73
<211> 46
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 73
gatcagcgct atccggatat agttcctcct ttcagcaaaa aacccc

46

<210> 74
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 74
gagcggccgc atgcaaaatc ggctgaccat c

31

<210> 75
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 75
gatcggggccc ttacttctgt aaccaccaga cagcctc

37

<210> 76
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 76
gatcggggccg cttagccggg aaacgtctgg cggc

34

<210> 77
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 77
gatcgtcgac tcaggcttc acatcactca ctgcacc 37

<210> 78
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 78
gatggatcca gcaaccgcac ctgtggc 27

<210> 79
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 79
gatgcgatcg ctatagttcc tcctttcagc aaaaaaccc 39

<210> 80
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 80
agctgagctc atgtgtggaa ttgttggcgc ga 32

<210> 81
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 81
tacgaagctt actcaaccgt aaccgatttt gc 32

<210> 82
<211> 34
<212> DNA
<213> Artificial sequence.

<220>
<223> primer

<400> 82
agctggtaacc atgtgtggaa tcgttaggtta tatc

34

<210> 83
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 83
tacgcatgct tactccacag taacactctt cgca

34

<210> 84
<211> 382
<212> PRT
<213> Escherichia coli

<400> 84

Met Tyr Ala Leu Thr Gln Gly Arg Ile Phe Thr Gly His Glu Phe Leu
1 5 10 15

Asp Asp His Ala Val Val Ile Ala Asp Gly Leu Ile Lys Ser Val Cys
20 25 30

Pro Val Ala Glu Leu Pro Pro Glu Ile Glu Gln Arg Ser Leu Asn Gly
35 40 45

Ala Ile Leu Ser Pro Gly Phe Ile Asp Val Gln Leu Asn Gly Cys Gly
50 55 60

Gly Val Gln Phe Asn Asp Thr Ala Glu Ala Val Ser Val Glu Thr Leu
65 70 75 80

Glu Ile Met Gln Lys Ala Asn Glu Lys Ser Gly Cys Thr Asn Tyr Leu
85 90 95

Pro Thr Leu Ile Thr Thr Ser Asp Glu Leu Met Lys Gln Gly Val Arg
100 105 110

Val Met Arg Glu Tyr Leu Ala Lys His Pro Asn Gln Ala Leu Gly Leu
115 120 125

His Leu Glu Gly Pro Trp Leu Asn Leu Val Lys Lys Gly Thr His Asn
130 135 140

Pro Asn Phe Val Arg Lys Pro Asp Ala Ala Leu Val Asp Phe Leu Cys
145 150 155 160

Glu Asn Ala Asp Val Ile Thr Lys Val Thr Leu Ala Pro Glu Met Val
165 170 175

Pro Ala Glu Val Ile Ser Lys Leu Ala Asn Ala Gly Ile Val Val Ser
180 185 190

Ala Gly His Ser Asn Ala Thr Leu Lys Glu Ala Lys Ala Gly Phe Arg
195 200 205

Ala Gly Ile Thr Phe Ala Thr His Leu Tyr Asn Ala Met Pro Tyr Ile
210 215 220

Thr Gly Arg Glu Pro Gly Leu Ala Gly Ala Ile Leu Asp Glu Ala Asp
225 230 235 240

Ile Tyr Cys Gly Ile Ile Ala Asp Gly Leu His Val Asp Tyr Ala Asn
245 250 255

Ile Arg Asn Ala Lys Arg Leu Lys Gly Asp Lys Leu Cys Leu Val Thr
260 265 270

Asp Ala Thr Ala Pro Ala Gly Ala Asn Ile Glu Gln Phe Ile Phe Ala
275 280 285

Gly Lys Thr Ile Tyr Tyr Arg Asn Gly Leu Cys Val Asp Glu Asn Gly
290 295 300

Thr Leu Ser Gly Ser Ser Leu Thr Met Ile Glu Gly Val Arg Asn Leu
305 310 315 320

Val Glu His Cys Gly Ile Ala Leu Asp Glu Val Leu Arg Met Ala Thr
325 330 335

Leu Tyr Pro Ala Arg Ala Ile Gly Val Glu Lys Arg Leu Gly Thr Leu
340 345 350

Ala Ala Gly Lys Val Ala Asn Leu Thr Ala Phe Thr Pro Asp Phe Lys
355 360 365

Ile Thr Lys Thr Ile Val Asn Gly Asn Glu Val Val Thr Gln
370 375 380

<210> 85
<211> 1149
<212> DNA
<213> Escherichia coli

<400> 85
atgtatgcat taaccaggc ccggatctt accggccacg aatttcttga tgaccacg 60
gttggtatcg ctgatggcct gattaaaagc gtctgtccgg tagcggact gcccgg 120
atcgaacaac gttcaactgaa cggggccatt ctctccccg gttttatcga tgtgcagtta 180
aacggctg 240
gcggcgtaca gtttaacgac accgctgaag cggtcagcgt ggaaacgctg 240
gaaatcatgc agaaagccaa tgagaaatca ggctgtacta actatctgcc gacgctt 300
accaccagcg atgagctgat gaaacaggc gtgcgcgtta tgcgcgagta cctggcaaaa 360
catccgaatc aggcgttagg tctgcattcg gaaggccgt ggctgaatct ggtaaaaaaa 420
ggcacccata atccgaattt tgtgcgtaaag cctgatgccg cgctggcga tttcctgtgt 480
gaaaacgccc acgtcattac caaagtgacc ctggcaccgg aaatggttcc tgccgg 540
atcagcaaac tggcaaattgc cgggattgtg gtttctgccg gtcactccaa cgccgacgtt 600
aaagaagccaa aagccgg 660
tttccgtata ttaccggcgtcg tgaacctggc ctggcggcgc cgatcctcga cgaagctgac 720
atttattgcgt gtattattgc tgatggctg catgttgcgtt acgccaacat tcgcaacgct 780
aaacgtctga aaggcgacaa actgtgtctg gttactgacg ccaccgcg 840
aacattgaac agttcatttt tgcgggtaaa acaatataact accgtaacgg actttgtgt 900
gatgagaacg gtacgttaag cggttcatcc ttaaccatga ttgaaggcgt gcgtaatctg 960
gtcgaacatt gcggatcgc actggatgaa gtgtacgta tggcgcacgct ctatccggc 1020
cgtgcgattt gcgttgagaa acgtctcggc acactcgccg caggtaaagt agccaaac 1080
actgcattca cacctgattt taaaatcacc aagaccatcg ttaacggtaa cgaggtcgta 1140
actcaataa 1149

<210> 86
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 86
gagcggccgc atgaatcaat cttatggacg gc

32

<210> 87
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 87
gagtcgactc agcgttgct gatctgatcg aacgtac

37

<210> 88
<211> 1410
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1410)
<223>

<400> 88
atg tcc gct gaa cac gta ctg acg atg ctg aac gag cac gaa gtg aag
Met Ser Ala Glu His Val Leu Thr Met Leu Asn Glu His Glu Val Lys
1 5 10 15

48

ttt gtt gat ttg cgc ttc acc gat act aaa ggt aaa gaa cag cac gtc
Phe Val Asp Leu Arg Phe Thr Asp Thr Lys Gly Lys Glu Gln His Val
20 25 30

96

act atc cct gct cat cag gtg aat gct gaa ttc ttc gaa gaa ggc aaa
Thr Ile Pro Ala His Gln Val Asn Ala Glu Phe Phe Glu Glu Gly Lys
35 40 45

144

atg ttt gac ggc tcc tcg att ggc ggc tgg aaa ggc att aac gag tcc
Met Phe Asp Gly Ser Ser Ile Gly Gly Trp Lys Gly Ile Asn Glu Ser
50 55 60

192

gac atg gtg ctg atg cca gac gca tcc acc gca gtg att gac ccg ttc
Asp Met Val Leu Met Pro Asp Ala Ser Thr Ala Val Ile Asp Pro Phe
65 70 75 80

240

ttc gcc gac tcc acc ctg att atc cgt tgc gac atc ctt gaa cct ggc
Phe Ala Asp Ser Thr Leu Ile Ile Arg Cys Asp Ile Leu Glu Pro Gly
85 90 95

288

acc ctg cca ggc tat gac cgt gac ccg cgc tcc att gcg aag cgc gcc
Thr Leu Gln Gly Tyr Asp Arg Asp Pro Arg Ser Ile Ala Lys Arg Ala
100 105 110

336

gaa gat tac ctg cgt tcc act ggc att gcc gac acc gta ctg ttc ggg

384

Glu Asp Tyr Leu Arg Ser Thr Gly Ile Ala Asp Thr Val Leu Phe Gly			
115	120	125	
cca gaa cct gaa ttc ttc ctg ttc gat gac atc cgt ttc gga tca tct			432
Pro Glu Pro Glu Phe Phe Leu Phe Asp Asp Ile Arg Phe Gly Ser Ser			
130	135	140	
atc tcc ggt tcc cac gtt gct atc gac gat atc gaa ggc gca tgg aac			480
Ile Ser Gly Ser His Val Ala Ile Asp Asp Ile Glu Gly Ala Trp Asn			
145	150	155	160
tcc tcc acc caa tac gaa ggt ggt aac aaa ggt cac cgt ccg gca gtg			528
Ser Ser Thr Gln Tyr Glu Gly Asn Lys Gly His Arg Pro Ala Val			
165	170	175	
aaa ggc ggt tac ttc ccg gtt cca ccg gta gac tcg gct cag gat att			576
Lys Gly Gly Tyr Phe Pro Val Pro Val Asp Ser Ala Gln Asp Ile			
180	185	190	
cgt tct gaa atg tgt ctg gtg atg gaa cag atg ggt ctg gtg gtt gaa			624
Arg Ser Glu Met Cys Leu Val Met Glu Gln Met Gly Leu Val Val Glu			
195	200	205	
gcc cat cac cac gaa gta gcg act gct ggt cag aac gaa gtg gct acc			672
Ala His His Glu Val Ala Thr Ala Gly Gln Asn Glu Val Ala Thr			
210	215	220	
cgc ttc aat acc atg acc aaa aaa gct gac gaa att cag atc tac aaa			720
Arg Phe Asn Thr Met Thr Lys Lys Ala Asp Glu Ile Gln Ile Tyr Lys			
225	230	235	240
tat gtt gtg cac aac gta gcg cac cgc ttc ggt aaa acc gcg acc ttt			768
Tyr Val Val His Asn Val Ala His Arg Phe Gly Lys Thr Ala Thr Phe			
245	250	255	
atg cca aaa ccg atg ttc ggt gat aac ggc tcc ggt atg cac tgc cac			816
Met Pro Lys Pro Met Phe Gly Asp Asn Gly Ser Gly Met His Cys His			
260	265	270	
atg tct ctg tct aaa aac ggc gtt aac ctg ttc gca ggc gac aaa tac			864
Met Ser Leu Ser Lys Asn Gly Val Asn Leu Phe Ala Gly Asp Lys Tyr			
275	280	285	
gca ggt ctg tct gag cag gcg ctg tac tac att ggc ggc gta atc aaa			912
Ala Gly Leu Ser Glu Gln Ala Leu Tyr Tyr Ile Gly Gly Val Ile Lys			
290	295	300	
cac gct aaa gcg att aac gcc ctg gca aac ccg acc acc aac tct tat			960
His Ala Lys Ala Ile Asn Ala Leu Ala Asn Pro Thr Thr Asn Ser Tyr			
305	310	315	320
aag cgt ctg gtc ccg ggc tat gaa gca ccg gta atg ctg gct tac tct			1008
Lys Arg Leu Val Pro Gly Tyr Glu Ala Pro Val Met Leu Ala Tyr Ser			
325	330	335	
gcg cgt aac cgt tct gcg tct atc cgt att ccg gtg gtt tct tct ccg			1056
Ala Arg Asn Arg Ser Ala Ser Ile Arg Ile Pro Val Val Ser Ser Pro			
340	345	350	

aaa gca cgt cgt atc gaa gta cgt ttc ccg gat ccg gca gct aac ccg Lys Ala Arg Arg Ile Glu Val Arg Phe Pro Asp Pro Ala Ala Asn Pro 355 360 365	1104
tac ctg tgc ttt gct gcc ctg ctg atg gcc ggt ctt gat ggt atc aag Tyr Leu Cys Phe Ala Ala Leu Leu Met Ala Gly Leu Asp Gly Ile Lys 370 375 380	1152
aac aag atc cat ccg ggc gaa gcc atg gac aaa aac ctg tat gac ctg Asn Lys Ile His Pro Gly Glu Ala Met Asp Lys Asn Leu Tyr Asp Leu 385 390 395 400	1200
ccg cca gaa gaa gcg aaa gag atc cca cag gtt gca ggc tct ctg gaa Pro Pro Glu Glu Ala Lys Glu Ile Pro Gln Val Ala Gly Ser Leu Glu 405 410 415	1248
gaa gca ctg aac gaa ctg gat ctg gac cgc gag ttc ctg aaa gcc ggt Glu Ala Leu Asn Glu Leu Asp Leu Asp Arg Glu Phe Leu Lys Ala Gly 420 425 430	1296
ggc gtg ttc act gac gaa gca att gat gcg tac atc gct ctg cgt cgc Gly Val Phe Thr Asp Glu Ala Ile Asp Ala Tyr Ile Ala Leu Arg Arg 435 440 445	1344
gaa gaa gat gac cgc gtg cgt atg act ccg cat ccg gta gag ttt gag Glu Glu Asp Asp Arg Val Arg Met Thr Pro His Pro Val Glu Phe Glu 450 455 460	1392
ctg tac tac agc gtc taa Leu Tyr Tyr Ser Val 465	1410
<210> 89	
<211> 469	
<212> PRT	
<213> Escherichia coli	
<400> 89	
Met Ser Ala Glu His Val Leu Thr Met Leu Asn Glu His Glu Val Lys 1 5 10 15	
Phe Val Asp Leu Arg Phe Thr Asp Thr Lys Gly Lys Glu Gln His Val 20 25 30	
Thr Ile Pro Ala His Gln Val Asn Ala Glu Phe Phe Glu Glu Gly Lys 35 40 45	
Met Phe Asp Gly Ser Ser Ile Gly Gly Trp Lys Gly Ile Asn Glu Ser 50 55 60	
Asp Met Val Leu Met Pro Asp Ala Ser Thr Ala Val Ile Asp Pro Phe 65 70 75 80	

Phe Ala Asp Ser Thr Leu Ile Ile Arg Cys Asp Ile Leu Glu Pro Gly
85 90 95

Thr Leu Gln Gly Tyr Asp Arg Asp Pro Arg Ser Ile Ala Lys Arg Ala
100 105 110

Glu Asp Tyr Leu Arg Ser Thr Gly Ile Ala Asp Thr Val Leu Phe Gly
115 120 125

Pro Glu Pro Glu Phe Phe Leu Phe Asp Asp Ile Arg Phe Gly Ser Ser
130 135 140

Ile Ser Gly Ser His Val Ala Ile Asp Asp Ile Glu Gly Ala Trp Asn
145 150 155 160

Ser Ser Thr Gln Tyr Glu Gly Gly Asn Lys Gly His Arg Pro Ala Val
165 170 175

Lys Gly Gly Tyr Phe Pro Val Pro Pro Val Asp Ser Ala Gln Asp Ile
180 185 190

Arg Ser Glu Met Cys Leu Val Met Glu Gln Met Gly Leu Val Val Glu
195 200 205

Ala His His His Glu Val Ala Thr Ala Gly Gln Asn Glu Val Ala Thr
210 215 220

Arg Phe Asn Thr Met Thr Lys Lys Ala Asp Glu Ile Gln Ile Tyr Lys
225 230 235 240

Tyr Val Val His Asn Val Ala His Arg Phe Gly Lys Thr Ala Thr Phe
245 250 255

Met Pro Lys Pro Met Phe Gly Asp Asn Gly Ser Gly Met His Cys His
260 265 270

Met Ser Leu Ser Lys Asn Gly Val Asn Leu Phe Ala Gly Asp Lys Tyr
275 280 285

Ala Gly Leu Ser Glu Gln Ala Leu Tyr Tyr Ile Gly Gly Val Ile Lys
290 295 300

His Ala Lys Ala Ile Asn Ala Leu Ala Asn Pro Thr Thr Asn Ser Tyr
305 310 315 320

Lys Arg Leu Val Pro Gly Tyr Glu Ala Pro Val Met Leu Ala Tyr Ser
325 330 335

Ala Arg Asn Arg Ser Ala Ser Ile Arg Ile Pro Val Val Ser Ser Pro
340 345 350

Lys Ala Arg Arg Ile Glu Val Arg Phe Pro Asp Pro Ala Ala Asn Pro
355 360 365

Tyr Leu Cys Phe Ala Ala Leu Leu Met Ala Gly Leu Asp Gly Ile Lys
370 375 380

Asn Lys Ile His Pro Gly Glu Ala Met Asp Lys Asn Leu Tyr Asp Leu
385 390 395 400

Pro Pro Glu Glu Ala Lys Glu Ile Pro Gln Val Ala Gly Ser Leu Glu
405 410 415

Glu Ala Leu Asn Glu Leu Asp Leu Asp Arg Glu Phe Leu Lys Ala Gly
420 425 430

Gly Val Phe Thr Asp Glu Ala Ile Asp Ala Tyr Ile Ala Leu Arg Arg
435 440 445

Glu Glu Asp Asp Arg Val Arg Met Thr Pro His Pro Val Glu Phe Glu
450 455 460

Leu Tyr Tyr Ser Val
465

<210> 90
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 90
gatcggcttc gcatgtccgc tgaacacgta ctgac

35

<210> 91
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 91
gatcctcgag ttagacgctg tagtacagct c

31

<210> 92
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 92
gatcgccgc ttacatgctg tagcccagc

29

<210> 93
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 93
gatcctgcag tcatgctgct aataatctat cc

32

<210> 94
<211> 1476
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1476)
<223>

<400> 94
atg gcg gta acg caa aca gcc cag gtc tgt gac ttg gtc att ttc ggc
Met Ala Val Thr Gln Thr Ala Gln Val Cys Asp Leu Val Ile Phe Gly
1 5 10 15

48

gcg aaa ggc gac ctt gcg cgt aaa ttg ctg cct tcc ctg tat caa
Ala Lys Gly Asp Leu Ala Arg Arg Lys Leu Leu Pro Ser Leu Tyr Gln
20 25 30

96

ctg gaa aaa gcc ggt cag ctc aac ccg gac acc cgg att atc ggc gta
Leu Glu Lys Ala Gly Gln Leu Asn Pro Asp Thr Arg Ile Ile Gly Val
35 40 45

144

ggg cgt gct gac tgg gat aaa gcg gca tat acc aaa gtt gtc cgc gag
Gly Arg Ala Asp Trp Asp Lys Ala Ala Tyr Thr Lys Val Val Arg Glu
50 55 60

192

gcg ctc gaa act ttc atg aaa gaa acc att gat gaa ggt tta tgg gac
Ala Leu Glu Thr Phe Met Lys Glu Thr Ile Asp Glu Gly Leu Trp Asp
65 70 75 80

240

acc ctg agc gca cgt ctg gat ttt tgt aat ctc gat gtc aat gac act	288
Thr Leu Ser Ala Arg Leu Asp Phe Cys Asn Leu Asp Val Asn Asp Thr	
85 90 95	
gct gca ttc agc cgt ctc ggc gcg atg ctg gat caa aaa aat cgt atc	336
Ala Ala Phe Ser Arg Leu Gly Ala Met Leu Asp Gln Lys Asn Arg Ile	
100 105 110	
acc att aac tac ttt gcc atg ccg ccc agc act ttt ggc gca att tgc	384
Thr Ile Asn Tyr Phe Ala Met Pro Pro Ser Thr Phe Gly Ala Ile Cys	
115 120 125	
aaa ggg ctt ggc gag gca aaa ctg aat gct aaa ccg gca cgc gta gtc	432
Lys Gly Leu Gly Glu Ala Lys Leu Asn Ala Lys Pro Ala Arg Val Val	
130 135 140	
atg gag aaa ccg ctg ggg acg tcg ctg gcg acc tcg cag gaa atc aat	480
Met Glu Lys Pro Leu Gly Thr Ser Leu Ala Thr Ser Gln Glu Ile Asn	
145 150 155 160	
gat cag gtt ggc gaa tac ttc gag gag tgc cag gtt tac cgt atc gac	528
Asp Gln Val Gly Glu Tyr Phe Glu Glu Cys Gln Val Tyr Arg Ile Asp	
165 170 175	
cac tat ctt ggt aaa gaa acg gtg ctg aac ctg ttg gcg ctg cgt ttt	576
His Tyr Leu Gly Lys Glu Thr Val Leu Asn Leu Leu Ala Leu Arg Phe	
180 185 190	
gct aac tcc ctg ttt gtg aat aac tgg gac aat cgc acc att gat cat	624
Ala Asn Ser Leu Phe Val Asn Asn Trp Asp Asn Arg Thr Ile Asp His	
195 200 205	
gtt gag att acc gtg gca gaa gaa gtg ggg atc gaa ggg cgc tgg ggc	672
Val Glu Ile Thr Val Ala Glu Glu Val Gly Ile Glu Gly Arg Trp Gly	
210 215 220	
tat ttt gat aaa gcc ggt cag atg cgc gac atg atc cag aac cac ctg	720
Tyr Phe Asp Lys Ala Gly Gln Met Arg Asp Met Ile Gln Asn His Leu	
225 230 235 240	
ctg caa att ctt tgc atg att gcg atg tct ccg ccg tct gac ctg agc	768
Leu Gln Ile Leu Cys Met Ile Ala Met Ser Pro Pro Ser Asp Leu Ser	
245 250 255	
gca gac agc atc cgc gat gaa aaa gtg aaa gta ctg aag tct ctg cgc	816
Ala Asp Ser Ile Arg Asp Glu Lys Val Lys Val Leu Lys Ser Leu Arg	
260 265 270	
cgc atc gac cgc tcc aac gta cgc gaa aaa acc gta cgc ggg caa tat	864
Arg Ile Asp Arg Ser Asn Val Arg Glu Lys Thr Val Arg Gly Gln Tyr	
275 280 285	
act gcg ggc ttc gcc cag ggc aaa aaa gtg ccg gga tat ctg gaa gaa	912
Thr Ala Gly Phe Ala Gln Gly Lys Val Pro Gly Tyr Leu Glu Glu	
290 295 300	
gag ggc gcg aac aag agc agc aat aca gaa acc ttc gtg gcg atc cgc	960
Glu Gly Ala Asn Lys Ser Ser Asn Thr Glu Thr Phe Val Ala Ile Arg	
305 310 315 320	

gtc gac att gat aac tgg cgc tgg gcc ggt gtg cca ttc tac ctg cgt	325	330	335	1008
Val Asp Ile Asp Asn Trp Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg				
act ggt aaa cgt ctg ccg acc aaa tgt tct gaa gtc gtg gtc tat ttc	340	345	350	1056
Thr Gly Lys Arg Leu Pro Thr Lys Cys Ser Glu Val Val Val Tyr Phe				
aaa aca cct gaa ctg aat ctg ttt aaa gag tcg tgg cag gat ctg ccg	355	360	365	1104
Lys Thr Pro Glu Leu Asn Leu Phe Lys Glu Ser Trp Gln Asp Leu Pro				
cag aat aaa ctg act atc cgt ctg caa cct gat gaa ggc gtg gat atc	370	375	380	1152
Gln Asn Lys Leu Thr Ile Arg Leu Gln Pro Asp Glu Gly Val Asp Ile				
cag gta ctg aat aaa gtt cct ggc ctt gac cac aaa cat aac ctg caa	385	390	395	1200
Gln Val Leu Asn Lys Val Pro Gly Leu Asp His Lys His Asn Leu Gln				
atc acc aag ctg gat ctg agc tat tca gaa acc ttt aat cag acg cat	405	410	415	1248
Ile Thr Lys Leu Asp Leu Ser Tyr Ser Glu Thr Phe Asn Gln Thr His				
ctg gcg gat gcc tat gaa cgt ttg ctg ctg gaa acc atg cgt ggt att	420	425	430	1296
Leu Ala Asp Ala Tyr Glu Arg Leu Leu Glu Thr Met Arg Gly Ile				
cag gca ctg ttt gta cgt cgc gat gaa gtg gaa gaa gcc tgg aaa tgg	435	440	445	1344
Gln Ala Leu Phe Val Arg Arg Asp Glu Val Glu Ala Trp Lys Trp				
gta gac tcc att act gag gcg tgg gcg atg gac aat gat gcg ccg aaa	450	455	460	1392
Val Asp Ser Ile Thr Glu Ala Trp Ala Met Asp Asn Asp Ala Pro Lys				
ccg tat cag gcc gga acc tgg gga ccc gtt gcc tcg gtg gcg atg att	465	470	475	1440
Pro Tyr Gln Ala Gly Thr Trp Gly Pro Val Ala Ser Val Ala Met Ile				
acc cgt gat ggt cgt tcc tgg aat gag ttt gag taa	485	490		1476
Thr Arg Asp Gly Arg Ser Trp Asn Glu Phe Glu				

<210> 95
 <211> 491
 <212> PRT
 <213> Escherichia coli

<400> 95

Met Ala Val Thr Gln Thr Ala Gln Val Cys Asp Leu Val Ile Phe Gly
 1 5 10 15

Ala Lys Gly Asp Leu Ala Arg Arg Lys Leu Leu Pro Ser Leu Tyr Gln
 20 25 30

Leu Glu Lys Ala Gly Gln Leu Asn Pro Asp Thr Arg Ile Ile Gly Val
35 40 45

Gly Arg Ala Asp Trp Asp Lys Ala Ala Tyr Thr Lys Val Val Arg Glu
50 55 60

Ala Leu Glu Thr Phe Met Lys Glu Thr Ile Asp Glu Gly Leu Trp Asp
65 70 75 80

Thr Leu Ser Ala Arg Leu Asp Phe Cys Asn Leu Asp Val Asn Asp Thr
85 90 95

Ala Ala Phe Ser Arg Leu Gly Ala Met Leu Asp Gln Lys Asn Arg Ile
100 105 110

Thr Ile Asn Tyr Phe Ala Met Pro Pro Ser Thr Phe Gly Ala Ile Cys
115 120 125

Lys Gly Leu Gly Glu Ala Lys Leu Asn Ala Lys Pro Ala Arg Val Val
130 135 140

Met Glu Lys Pro Leu Gly Thr Ser Leu Ala Thr Ser Gln Glu Ile Asn
145 150 155 160

Asp Gln Val Gly Glu Tyr Phe Glu Glu Cys Gln Val Tyr Arg Ile Asp
165 170 175

His Tyr Leu Gly Lys Glu Thr Val Leu Asn Leu Leu Ala Leu Arg Phe
180 185 190

Ala Asn Ser Leu Phe Val Asn Asn Trp Asp Asn Arg Thr Ile Asp His
195 200 205

Val Glu Ile Thr Val Ala Glu Glu Val Gly Ile Glu Gly Arg Trp Gly
210 215 220

Tyr Phe Asp Lys Ala Gly Gln Met Arg Asp Met Ile Gln Asn His Leu
225 230 235 240

Leu Gln Ile Leu Cys Met Ile Ala Met Ser Pro Pro Ser Asp Leu Ser
245 250 255

Ala Asp Ser Ile Arg Asp Glu Lys Val Lys Val Leu Lys Ser Leu Arg
260 265 270

Arg Ile Asp Arg Ser Asn Val Arg Glu Lys Thr Val Arg Gly Gln Tyr

275

280

285

Thr Ala Gly Phe Ala Gln Gly Lys Lys Val Pro Gly Tyr Leu Glu Glu

290

295

300

Glu Gly Ala Asn Lys Ser Ser Asn Thr Glu Thr Phe Val Ala Ile Arg

305

310

315

320

Val Asp Ile Asp Asn Trp Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg

325

330

335

Thr Gly Lys Arg Leu Pro Thr Lys Cys Ser Glu Val Val Val Tyr Phe

340

345

350

Lys Thr Pro Glu Leu Asn Leu Phe Lys Glu Ser Trp Gln Asp Leu Pro

355

360

365

Gln Asn Lys Leu Thr Ile Arg Leu Gln Pro Asp Glu Gly Val Asp Ile

370

375

380

Gln Val Leu Asn Lys Val Pro Gly Leu Asp His Lys His Asn Leu Gln

385

390

395

400

Ile Thr Lys Leu Asp Leu Ser Tyr Ser Glu Thr Phe Asn Gln Thr His

405

410

415

Leu Ala Asp Ala Tyr Glu Arg Leu Leu Glu Thr Met Arg Gly Ile

420

425

430

Gln Ala Leu Phe Val Arg Arg Asp Glu Val Glu Glu Ala Trp Lys Trp

435

440

445

Val Asp Ser Ile Thr Glu Ala Trp Ala Met Asp Asn Asp Ala Pro Lys

450

455

460

Pro Tyr Gln Ala Gly Thr Trp Gly Pro Val Ala Ser Val Ala Met Ile

465

470

475

480

Thr Arg Asp Gly Arg Ser Trp Asn Glu Phe Glu

485

490

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32

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37

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<223> primer

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27

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<400> 99

cacagtgtgc cgatgatttt gacc

24

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gatgctagct aaccggagct catagggc		28
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Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln		
1 5 10 15		
aaa cac ttc gat gaa atg aaa gac gtt acg atc gcc gat ctt ttt gct		96
Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala		
20 25 30		
aaa gac ggc gat cgt ttt tct aag ttc tcc gca acc ttc gac gat cag		144
Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln		
35 40 45		
atg ctg gtg gat tac tcc aaa aac cgc atc act gaa gag acg ctg gcg		192
Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala		

50	55	60	
aaa tta cag gat ctg gcg aaa gag tgc gat ctg gcg ggc gcg att aag Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys 65 : 70 75 80			240
tcg atg ttc tct ggc gag aag atc aac cgc act gaa aac cgc gcc gtg Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val 85 90 95			288
ctg cac gta gcg ctg cgt aac cgt agc aat acc ccg att ttg gtt gat Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp 100 105 110			336
ggc aaa gac gta atg ccg gaa gtc aac gcg gtg ctg gag aag atg aaa Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys 115 120 125			384
acc ttc tca gaa gcg att att tcc ggt gag tgg aaa ggt tat acc ggc Thr Phe Ser Glu Ala Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly 130 135 140			432
aaa gca atc act gac gta gtg aac atc ggg atc ggc ggt tct gac ctc Lys Ala Ile Thr Asp Val Val Asn Ile Gly Ile Gly Gly Ser Asp Leu 145 150 155 160			480
ggc cca tac atg gtg acc gaa gct ctg cgt ccg tac aaa aac cac ctg Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu 165 170 175			528
aac atg cac ttt gtt tct aac gtc gat ggg act cac atc gcg gaa gtg Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val 180 185 190			576
ctg aaa aaa gta aac ccg gaa acc acg ctg ttc ttg gta gca tct aaa Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys 195 200 205			624
acc ttc acc act cag gaa act atg acc aac gcc cat agc gcg cgt gac Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp 210 215 220			672
tgg ttc ctg aaa gcg gca ggt gat gaa aaa cac gtt gca aaa cac ttt Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe 225 230 235 240			720
gcg gcg ctt tcc acc aat gcc aaa gcc gtt ggc gag ttt ggt att gat Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp 245 250 255			768
act gcc aac atg ttc gag ttc tgg gac tgg gtt ggc ggc cgt tac tct Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser 260 265 270			816
ttg tgg tca gcg att ggc ctg tcg att gtt ctc tcc atc ggc ttt gat Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp 275 280 285			864
aac ttc gtt gaa ctg ctt tcc ggc gca cac gac gcg atg gac aag cat ttc			912

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe			
290	295	300	
tcc acc acg cct gcc gag aaa aac ctg cct gta ctg ctg gcg ctg att			960
Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile			
305	310	315	320
ggc atc tgg tac aac aat ttc ttt ggt gcg gaa act gaa gcg att ctg			1008
Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu			
325	330	335	
ccg tat gac cag tat atg cac cgt ttc gcg gcg tac ttc cag cag ggc			1056
Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly			
340	345	350	
aat atg gag tcc aac ggt aag tat gtt gac cgt aac ggt aac gtt gtg			1104
Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val			
355	360	365	
gat tac cag act ggc ccg att atc tgg ggt gaa cca ggc act aac ggt			1152
Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly			
370	375	380	
cag cac gcg ttc tac cag ctg atc cac cag gga acc aaa atg gta ccg			1200
Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro			
385	390	395	400
tgc gat ttc atc gct ccg gct atc acc cat aac ccg ctc tct gat cat			1248
Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His			
405	410	415	
cac cag aaa ctg ctg tct aac ttc ttc gcc cag acc gaa gcg ctg gcg			1296
His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala			
420	425	430	
ttt ggt aaa tcc cgc gaa gtg gtt gag cag gaa tat cgt gat cag ggt			1344
Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly			
435	440	445	
aaa gat ccg gca acg ctt gac tac gtg gtg ccg ttc aaa gta ttc gaa			1392
Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu			
450	455	460	
ggt aac cgc ccg acc aac tcc atc ctg ctg cgt gaa atc act ccg ttc			1440
Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe			
465	470	475	480
agc ctg ggt gcg ttg att gcg ctg tat gag cac aaa atc ttt act cag			1488
Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln			
485	490	495	
ggc gtg atc ctg aac atc ttc acc ttc gac cag tgg ggc gtg gaa ctg			1536
Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu			
500	505	510	
ggt aaa cag ctg gcg aac cgt att ctg cca gag ctg aaa gat gat aaa			1584
Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys			
515	520	525	

gaa atc agc agc cac gat agc tcg acc aat ggt ctg att aac cgc tat 1632
Glu Ile Ser Ser His Asp Ser Ser Thr Asn Gly Leu Ile Asn Arg Tyr
530 535 540

aaa gcg tgg cgc ggt taa 1650
Lys Ala Trp Arg Gly
545

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<211> 549
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<400> 105

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
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Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
130 135 140

Lys Ala Ile Thr Asp Val Val Asn Ile Gly Ile Gly Gly Ser Asp Leu
145 150 155 160

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys
515 520 525

Glu Ile Ser Ser His Asp Ser Ser Thr Asn Gly Leu Ile Asn Arg Tyr
530 535 540

Lys Ala Trp Arg Gly
545

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gatcctcag ttaaccgcgc cacgctttat agc 33

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<400> 108
ggatcctacc tgacgctttt tatcgcaact c 31

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cgggacgcaca tcggccctcggt agac 24

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gattccggaa gcaaccgcac ctgtggc 27

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gatcacacctgg ttatagttcc tcctttcagc aaaaaaacc 39

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<400> 112
gagtcatccg gatacagttac gcga 24

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<400> 113
ataaaaccagc cgggcaaatg g

21

<210> 114
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<400> 114
cgccaaagctt ggtaccg

17

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ccctctagat gcatgctcga g

21

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attgtgcgt cagtatagga agg

23

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cgataactgac gggctccag

19

<210> 118
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gcaaaaacctt tcgcggcac ccatgatagc gcccg 35

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ccaccatgat attcggcaag cag 23

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21

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gtcagagaag tcgttcttag cgatg

25

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ggatctaaac ctcagtacg accggtag aactatgt

38

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38

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cacgcaggca ggcttacct tcttc

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24

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agggcatcgt tcccactgct atgctggttg ccaacgatca gatggcgctg ggcgcaatgc	240	
gcccattac cgagtccggg ctgcgcgttg gtgcggatat ctcggtagtg ggatacgcacg	300	
ataccgaaga cagctcatgt tatatccgc cgttaaccac catcaaacag gattttcgcc	360	
tgctgggca aaccagctg gaccgcttgc tgcaactctc tcagggccag gcggtgaagg	420	
gcaatcagct gttccccgtc tcactggta aaagaaaaac caccctggcg cccaaatacgc	480	
aaaccgcctc tccccgcgc ttggccgatt cattaatgca gctggcacga caggttccc	540	
gactggaaag cgggcagtga ggcacacgca attaatgtga gttagctcac tcattaggca	600	
ccccaggctt tacactttat gttccggct cgtatgtgt gtgaaattgt gagcggataa	660	
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ggcggcttaa aatgcctgatg

23

<210> 137
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28